

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraphs at page 6, lines 22-27 with the following rewritten paragraphs:

-- **Figures 7A-7H** show the cDNA sequence (SEQ ID NO: 19) and amino acid sequence (SEQ ID NO: 111) of Gene 454 with the corresponding SNPs underlined.

Figure 8 shows the results of RT-PCR analysis of Gene 561.1 and Gene 561.2.

Figures 9A-9F show the cDNA sequence (SEQ ID NO: 90) and amino acid sequence (SEQ ID NO: 153) of Gene 757 with the corresponding SNPs underlined. --

Please replace the paragraphs at page 9, lines 3-6 with the following rewritten paragraphs:

-- **Figures 27A-27K** show the cDNA sequence (SEQ ID NO: 30) and amino acid sequence (SEQ ID NO: 120) of Gene 561.1 with the corresponding SNPs underlined.

Figures 28A-28C show the cDNA sequence (SEQ ID NO: 32) and amino acid sequence (SEQ ID NO: 121) of Gene 561.2 with the corresponding SNPs underlined. --

Please replace line 21 at page 49 with the following rewritten line:

-- NO: 6160), GLU-GLU, and DYKDDDDK (SEQ ID NO: 4688) (FLAG®) epitope tags. --

Please replace Table 2 on pages 128-137 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 2: PRIMER PAIRS

Marker name	Locus	DNA type	Gene	Forward primer	Seq ID NO.	Reverse primer	Seq ID NO.
B0610N03-A1 x		BACend		CAAGCGATAGTTCTAATTTCT	<u>4689</u>	TATGTGTGAGCCAGAAAAAT	<u>4714</u>
B0600D18-A2 x		BACend		TGGTGTCTCTGAGCTTCAGG	<u>4690</u>	ACCGAACCCAAAGATCCTGGAA	<u>4715</u>
B0610I14-A2 x		BACend		GTCCTGATTTAAGGTTTGAGG	<u>4691</u>	CTGCCCTCACC TTGCCCTCAAC	<u>4716</u>
B0700A09-A2 x		BACend		GCTGCTTCAGGCATTTACAGCAT	<u>4692</u>	CAGTGTATATGTGATGCTGAA	<u>4717</u>
B0716I10-A2 x		BACend		ATGATGCAGTGAGTGAGACCCA	<u>4693</u>	CTTACTCACTACACTGGGTCCTC	<u>4718</u>
B1118B13-A2 x		BACend		GCACGTGGGTCCTCTCATCTGCT	<u>4694</u>	ACTCTCGTGGATAGAGCAGATG	<u>4719</u>
B1128N10-A2 x		BACend		CACGAGAGTCTAGTGGGGGTTT	<u>4695</u>	TCACCTGGCAGATGAAACCCCC	<u>4720</u>
B0841C17-A2 x		BACend		TCCCTGATATCCACTATCTTT	<u>4696</u>	CATTAGATGATGGTAAAGATAG	<u>4721</u>
B0904G06-A2 x		BACend		ACTGTCTCATTTCTTACAGAAA	<u>4697</u>	GGAACAGCAAACGTTTCTGTGA	<u>4722</u>
B0923J13-A2 x		BACend		CAGGTCTCTGCAGAGCAATTTCT	<u>4698</u>	GACTCTTGTTAACGAGAAATGC	<u>4723</u>
B0675M15-A2 x		BACend		GCAGACAATATCAAGAGTTCTT	<u>4699</u>	CTGTAACACATCTCAAGAAGCTC	<u>4724</u>
B0600D18-A2 y		BACend		TCATCTGCCAAGTGAGCCCACT	<u>4700</u>	GACCTCACCAAAGCACTGGGCT	<u>4725</u>
B0610N03-A2 y		BACend		GATACCAATGTGAAGTCCTTGA	<u>4701</u>	GTTTTCTTCCAGCCTCAAGGAC	<u>4726</u>
B0700A09-A2 y		BACend		TCTCGATCCCACTAACCCAGAT	<u>4702</u>	ATGAAGTACATTTGGATCGTGGT	<u>4727</u>
B1118B13-A2 y		BACend		ACTGGAATGCTCAGCTGATGC	<u>4703</u>	TTCTCCAGGGTCAAGCATCCAG	<u>4728</u>
B1128N10-A2 y		BACend		TGCTGATCTCTCAGTTCAACCT	<u>4704</u>	GCAAGCCACCCCATCAGGGTGAA	<u>4729</u>
B0904G06-A2 y		BACend		ATCTAATGCTGTGCCCGCTGCT	<u>4705</u>	GGTTTGTTTGCTGCAGCAGCGG	<u>4730</u>
B0923J13-A2 y		BACend		GACAGCCAGAGGAAACCTCTTTC	<u>4706</u>	AAAAGTTGTCCTTGGGAAGAGT	<u>4731</u>
B0675M15-A2 y		BACend		CACCTCTGGCTTTCCTACCAACC	<u>4707</u>	AGCTGTGACATGAAGGTTGTAG	<u>4732</u>
B0635H04-A1 x		BACend		AGCTTCGTCTGACCAGTCTACC	<u>4708</u>	TTCAGGAACCAACCAAGGTAGACT	<u>4733</u>
B0666B20-A1 x		BACend		TGCCCTGTGACTGAAGTCTTGAT	<u>4709</u>	GAGTGAGTAAGGAATCAAGAC	<u>4734</u>
B0696D03-A1 x		BACend		AGGAAGAACAAGAACGATCTTT	<u>4710</u>	GTCATTATTTCCTCAAAAGACTG	<u>4735</u>
B0700H07-A1 x		BACend		TCCTGGGAAGCAAGAAATAGGAA	<u>4711</u>	TCGCAGTGGCTTTGTTCTATT	<u>4736</u>
B0726A20-A1 x		BACend		ACTGTTGTCAACCTCTGGGAAAG	<u>4712</u>	AGTCTTCAGGTCCTCTTTCCCA	<u>4737</u>
B0761L21-A1 x		BACend		GAGTAAAGAATGTGTATAGGG	<u>4713</u>	TTTTTTGACCCACCCCTATAC	<u>4738</u>
B0814G06-A1 x		BACend		CGAGGAAGATGTAAGAGACTGT	<u>4739</u>	ATTGAGGCCCCAGAACAGTCTC	<u>4768</u>
B0857A05-A1 x		BACend		TCCTTAGTCCCTTTGGAGAGCT	<u>4740</u>	ATTTTCCACAGAGGAAGCTCTCC	<u>4769</u>
B0895C23-A1 x		BACend		AGGTGCTACCTCGCTCAATCTG	<u>4741</u>	GGGCTGGTTGCTCACAGATTGA	<u>4770</u>
B0949E15-A1 x		BACend		CTTTTGAAGACGTGGGTTCTGT	<u>4742</u>	GAA TGCAAGCACTCACAGAAC	<u>4771</u>
B0604M16-A1 x		BACend		AGCCATAAACACACATTTCTAT	<u>4743</u>	GATGCTCTGTGATATAGAAAT	<u>4772</u>

B0615D12-A1 x	BACend	TCCACTGAGAGTTACCAAACCC	<u>4744</u>	GGTATGAGAAITGTGGGTTTG	<u>4773</u>
B0633K01-A1 x	BACend	GTTCAGATTTTATCTTGGGTAT	<u>4745</u>	ACTGATGACATTTGATACCCAA	<u>4774</u>
B0663H23-A1 x	BACend	GAGGTCCCTATTGCTGTGTTTT	<u>4746</u>	CAGCCAAATGAAGTCAAAACACA	<u>4775</u>
B0696L08-A1 x	BACend	ATCTGTAGCCTATAGTGAACAG	<u>4747</u>	TTTACAGTGTTTGCCCTGTTTAC	<u>4776</u>
B0702C13-A1 x	BACend	GTAGTAACAGAAITGACITTTGA	<u>4748</u>	AGAGAGGAACAGCATCAAAAGTC	<u>4777</u>
B0702F18-A1 x	BACend	CTCTGCATTTCTTACTCCTTAC	<u>4749</u>	AAGCTTTACTACCAGTAAGGAG	<u>4778</u>
B0728K24-A1 x	BACend	TCGCAAAATAGCACCAAGGGACTT	<u>4750</u>	CACCGTTATGCAAGAAAGTCCCT	<u>4779</u>
B0738O20-A1 x	BACend	TGAAGTTGGAAATCCCTGATAG	<u>4751</u>	AGGTTCCCTACTGAGCTATCAGG	<u>4780</u>
B0866B05-A1 x	BACend	AGCAGAAGAGCAGACCCCTTCAA	<u>4752</u>	GGAGCATCCAATCTTTGAAGGG	<u>4781</u>
B0598D10-A1 y	BACend	AGATGCTTATACTTGGTGAAG	<u>4753</u>	TACTTACACAGTTGCTTACACC	<u>4782</u>
B0635H04-A1 y	BACend	AGTCACACCTTATGAGGCATCA	<u>4754</u>	CTGTATGAATCCTCTGATGCCCT	<u>4783</u>
B0666B20-A1 y	BACend	ATCCTGCTTTGTGGGTAGCCAC	<u>4755</u>	AAATGCCACGGTGCAGTGGCTAC	<u>4784</u>
B0700H07-A1 y	BACend	ACTCAAACCAACCCTTCCATTCA	<u>4756</u>	GGTTAGGATTAGTGTGAATGA	<u>4785</u>
B0726A20-A1 y	BACend	TCAGTTCTCAGTCCCTAGGAGAC	<u>4757</u>	GGTCTTCTACTCCAGTCTCCTA	<u>4786</u>
B0761L21-A1 y	BACend	GGGAGGCCCTGCTGTCTTTCTCA	<u>4758</u>	AAATTAGCCAGGCAITGAGAAAG	<u>4787</u>
B0814G06-A1 y	BACend	GCAGAGAGGTGGTGAAGTGCAATC	<u>4759</u>	TGACAGTTTTCCTTTGATGCACT	<u>4788</u>
B0857A05-A1 y	BACend	TGCTTATCAAGATGCCCTTTGCC	<u>4760</u>	AATCAGGCCATGAGGGCAAAAGG	<u>4789</u>
B0895C23-A1 y	BACend	CCATCCTTCATCCCCAGCAGTA	<u>4761</u>	CCCTGAAITTAGGTTACTGCTG	<u>4790</u>
B0931G12-A1 y	BACend	AGAACCAAGGCAGAGCTACCTGG	<u>4762</u>	CTGGACCAGGAAATCCAGGTTAG	<u>4791</u>
B0949E15-A1 y	BACend	ACTAGCTATTGAAGTGACTATC	<u>4763</u>	ATGGGCAAAAGAAATAGATAGTCA	<u>4792</u>
B0604M16-A1 y	BACend	GTTTCAGCTGTGAAAAATGTTA	<u>4764</u>	TGCTTTCCTCCCTTAACATTT	<u>4793</u>
B0633K01-A1 y	BACend	ATGCTGCTTCATATTAACACATT	<u>4765</u>	CGGGAAGCAITTTGCCAATGTGTT	<u>4794</u>
B0663H23-A1 y	BACend	CTCGCTCCATCTGCGATGCACA	<u>4766</u>	AGGTGATCACAGACTGTGCATC	<u>4795</u>
B0696L08-A1 y	BACend	TGTTGTGTCAAGAACTCAGGAA	<u>4767</u>	ACCCAGCTGAATCCTTCTGAG	<u>4796</u>
B0702C13-A1 y	BACend	TCATGGGGGTGCTTTGACCCTTG	<u>4797</u>	TGGCCTCAAAAGGCTCAAGGTCA	<u>4826</u>
B0702F18-A1 y	BACend	CATGGTCAACCTGCAGCCCTCTCA	<u>4798</u>	TGGCTAGAAAGGAGGTGAGAGGC	<u>4827</u>
B0738O20-A1 y	BACend	AGAAAGCGGGGTGAGCAGGACAT	<u>4799</u>	GTTACCCCGGAGTTATGTCTG	<u>4828</u>
B0866B05-A1 y	BACend	GATGTTGTCCGACAGGCATGGG	<u>4800</u>	TTCCGTGTAGATCCCCATGGCC	<u>4829</u>
B0883G23-A1 y	BACend	GTGGTAGAAITGGCAAGCCTTG	<u>4801</u>	CTCCAATCAGTTGCCAAGGCTT	<u>4830</u>
B0909L16-A1 y	BACend	GGTAAGGACACCTTCAAGGGAC	<u>4802</u>	TGGAGTGCCCTGTTGTCCCTTG	<u>4831</u>
B0974M10-A1 x	BACend	ATGCAAAAGGTCCTCAGGACGAAA	<u>4803</u>	CCCTTCCCTGACCAATTTCTGCC	<u>4832</u>
B1118L08-A1 x	BACend	GGCATGTAGATCAAAATGAATA	<u>4804</u>	TGCTCCTAGCTGAATATTTCAT	<u>4833</u>
B0723P10-A1 x	BACend	GGTAGCAGTCTTACACTGCTGG	<u>4805</u>	CCTTTCCGATGACCCCAAGCAGT	<u>4834</u>
B0748H09-A1 x	BACend	TGCCATGTAACGTTCAATATTCC	<u>4806</u>	GTTTTCTGTGCAAGGGAATATG	<u>4835</u>

B0825F09-A1.x		BACend		ATACCACAGGGTAGTAACAGT	<u>4807</u>	TTGTGGCTCAAAATCACTGTTAC	<u>4836</u>
B0825K21-A1.x		BACend		CGTGAGCCCATTTCAACCACAC	<u>4808</u>	TCCTGTCTTTGAAGTGTGTT	<u>4837</u>
B0845N16-A1.x		BACend		ACATATGAAAAAGACCGTAGAAA	<u>4809</u>	CAATTACAGGCACCTTTCTACG	<u>4838</u>
B0894N08-A1.x		BACend		ACGTGGAGAAAGCCGCTGTCTT	<u>4810</u>	CTGGACATTGAATAAGACAGC	<u>4839</u>
B0956I11-A1.x		BACend		TGAATTTTAAACAGGTGGCAAG	<u>4811</u>	ATTCATCTGACAGCTTTGCCA	<u>4840</u>
B0974M10-A1.y		BACend		CTCATAGTTGTTACACACTCTG	<u>4812</u>	AAGCACGTGTTGAACAGAGTGT	<u>4841</u>
B0646E20-A1.y		BACend		CTCCATAGGAAGCAGCCATCAG	<u>4813</u>	ACTGGACCCAGCAACTGATGGC	<u>4842</u>
B0723P10-A1.y		BACend		TGTACCAAACTGTTGACTATTA	<u>4814</u>	GTTGGCTCATGCTTAATAGTC	<u>4843</u>
B0748H09-A1.y		BACend		GCCTGCACAGGACACCAATTGCA	<u>4815</u>	TTCCGGGTTTGATGTGCAATTG	<u>4844</u>
B0825K21-A1.y		BACend		CAATAATTAGTTCCAATGGCGC	<u>4816</u>	CACAGTCAGAGTTGGCCCAATT	<u>4845</u>
B0845N16-A1.y		BACend		GAGTGTCAACCGGAAGAGAAGA	<u>4817</u>	TCCAGAGCCAACTGTCTTCTCT	<u>4846</u>
B0894N08-A1.y		BACend		TGCCTTTCTTCCITAGAGCTCC	<u>4818</u>	CATCTGGATTAGCTGGAGCTCT	<u>4847</u>
B0956I11-A1.y		BACend		TGTGGGATGCTTCCAGTTTTGT	<u>4819</u>	GATGAGTAGATCCCAACAAACT	<u>4848</u>
B0961F22-A1.x		BACend		CATCTGCCCTCGGGTCTGAACT	<u>4820</u>	GGTCACTGCAGGAAAGTTCAGA	<u>4849</u>
B0588P16-A1.x		BACend		AAGAAGGACCTCAACCAAGAGC	<u>4821</u>	ACCCATGTGTGTACAGCTCTTGG	<u>4850</u>
B1000B21-A1.x		BACend		TATTACAGAGGCGTGGTGATCAG	<u>4822</u>	TAGCCTGTACAGAAAGCTGATCAC	<u>4851</u>
B0839D11-A1.x		BACend		GACAACCTTGCTTCCTTTACCTG	<u>4823</u>	AGATGACCTATTGCCAGGTAAA	<u>4852</u>
B1052D15-A1.x		BACend		CAGAAGCATAGAAAACAATCCAG	<u>4824</u>	GCACTGTTTTATTAACCTGGATTG	<u>4853</u>
B1093F08-A1.x		BACend		TGCTGCAACTGCCAAAAGAATTG	<u>4825</u>	CCCTGGCGTTGCAGGAATTCTT	<u>4854</u>
B1134M23-A1.x		BACend		GAA TGCGGAGAAAGGGCAAAAG	<u>4855</u>	GCTCGTTAAGAGTTCTTTGCC	<u>4884</u>
B0894M06-A1.x		BACend		TCCTTCATCTCTCTAATGGGCAC	<u>4856</u>	TGGGTACATGCACGTGTGCCAT	<u>4885</u>
B0895J20-A1.x		BACend		ACAGACACCTTGGGTCAITGACT	<u>4857</u>	GGAAC TGGA TGTAAGTCATGA	<u>4886</u>
B0961F22-A1.y		BACend		CAGTGCTCCCTCTCTCATGAGT	<u>4858</u>	CTGCTTCTAGAACAACTCATGA	<u>4887</u>
B0668P23-A1.y		BACend		ACATGATGCACCCCTTACCGTT	<u>4859</u>	CCGTCGTGTGCCAGAACGGTAA	<u>4888</u>
B0588P16-A1.y		BACend		ACATGGGCTCACAGGAAGATCT	<u>4860</u>	CACGACTTAGGAGGAGATCTTC	<u>4889</u>
B1000B21-A1.y		BACend		AAGAGAACTGGGAGACTGTGTC	<u>4861</u>	TAGCAAGTCTTATCGACACAGT	<u>4890</u>
B0839D11-A1.y		BACend		CCACTCAACCCACAATCTAGTC	<u>4862</u>	GAATACAGGGGATGGGACTAGAT	<u>4891</u>
B1052D15-A1.y		BACend		CCACCMAATGGA TCTGTTGACT	<u>4863</u>	ATCAGAGGCTCTGTAAGTCAACA	<u>4892</u>
B1093F08-A1.y		BACend		AGGCCGGTTTCTTACTACAGAA	<u>4864</u>	TCGAAACAGCTGCC TTTCTGTAG	<u>4893</u>
B1134M23-A1.y		BACend		ACAGAAAGGGCGGTGGGTAGAGA	<u>4865</u>	TTCTTCATTCACGCTCTTACC	<u>4894</u>
B0894M06-A1.y		BACend		CACATCGCTGTCTGACAGAACT	<u>4866</u>	GGGTCA TG TGACTGAGTTCTGT	<u>4895</u>
B0895J20-A1.y		BACend		CACATTTCTGAGACACTTGCTA	<u>4867</u>	TAATACCTGGCATGTAGCAAGT	<u>4896</u>
B0604N13-A1.x		BACend		ATGAGTCTCTCCACCGAATGTG	<u>4868</u>	GAACCTCAGTCCCTGCACATTGG	<u>4897</u>
B0714L01-A1.x		BACend		TCATCAGTTCTAGGAGCTTTCA	<u>4869</u>	GTAAGTACTCTCTCTGAAAAGCT	<u>4898</u>

B0754A14-A1 x	BACend		GGATCGCACAGTCACTCTTCAT	<u>4870</u>	TGCAAGCGGATATGATGAAGAG	<u>4899</u>
B0894M06-A1 x	BACend		GATTAGTGTATGTAGAGACA	<u>4871</u>	TGGTGACGATTGTTGTCCTCT	<u>4900</u>
B1128L12-A1 x	BACend		TTGGTGTGAATCAAGCATCAGG	<u>4872</u>	TGAGCACAGGAGTTCCTGATGC	<u>4901</u>
B0643F18-A1 y	BACend		GTGGATTAAACCGAGGTGGAAT	<u>4873</u>	CCTTTCCAGTTTGAATTCCACC	<u>4902</u>
B0714L01-A1 y	BACend		GGCATTCTTGCTGCTGCTCTG	<u>4874</u>	GAATACTGCAGAAGCAGAAGCA	<u>4903</u>
B0754A14-A1 y	BACend		ATCCTGGGCAAGGGAGTTTCAG	<u>4875</u>	CTGAGCCACACCCTTCTGAACT	<u>4904</u>
B0894M06-A1 y	BACend		TTGTTACATCGCTGCTTGACA	<u>4876</u>	ATGTGACTGAGTTCTGTCAAGC	<u>4905</u>
B1128L12-A1 y	BACend		GCTTGAAC TGCACTCAGCAGGA	<u>4877</u>	GTGCTTCTAAGTTCTCTGCTG	<u>4906</u>
B0687F10-A1 x	BACend		TCTCTCAAGCCACTTTCATGT	<u>4878</u>	ACGTGAATCACCGGAACATAGAA	<u>4907</u>
B0791C09-A1 x	BACend		ACTGTGGCTGCACATAGGGATA	<u>4879</u>	AAAGCTTCCTGGGGTATCCCTA	<u>4908</u>
B0820N16-A1 x	BACend		GGACCCACCCCTGTCAATTTCA	<u>4880</u>	GGGGCGATGGGAATATGAATTT	<u>4909</u>
B0880M22-A1 x	BACend		TGTTTGGATA TGCTGGCTACTA	<u>4881</u>	TGTGTGTTTTGAGTTAGTAGCC	<u>4910</u>
B1008L21-A1 x	BACend		ATCTCTGGGAAGCTCTACAGTG	<u>4882</u>	CTCAAAATCCCTCCCACTGTAG	<u>4911</u>
B1043N20-A1 x	BACend		AGATAATGGGTTGCTTGGGCTC	<u>4883</u>	GTTAAAGCAGTTATGAGCCCAA	<u>4912</u>
B0700H07-A2 x	BACend		CTTGACCTCAAGACATCCTCTG	<u>4913</u>	TGGGAGACTGAGACCAGAGGAT	<u>4942</u>
B0687F10-A1 y	BACend		TTTCAGTGACTGCTCTTCCGTT	<u>4914</u>	TGGCTGTAAGTGAAACGGAAG	<u>4943</u>
B0791C09-A1 y	BACend		CATTAGAAGCCCAAGAGGAAC	<u>4915</u>	CTCCTTCTTCCCGAGTTTCTCTC	<u>4944</u>
B0880M22-A1 y	BACend		CTATGTTGCATAGGAGTAGTGA	<u>4916</u>	AAGGATACCCCTCTCTCACTACT	<u>4945</u>
B0909E24-A1 y	BACend		CCCTCTATAACATTTTCTCCA	<u>4917</u>	CTTAGGACAACCCCTGGGAGAA	<u>4946</u>
B1008L21-A1 y	BACend		GAGCCCTGCTCAGAAITTCATG	<u>4918</u>	GAGGCAAGGTCITTCATGAAT	<u>4947</u>
B0923H14-A1 y	BACend		GCAGCCTTACTGAGCTGACAGT	<u>4919</u>	CCGTCCATGGGAACACTGTACG	<u>4948</u>
B0979G13-A1 y	BACend		CTCCACCITGATGGGTCAACTT	<u>4920</u>	ATTAAGTTCCCTTGAAGGTTGAC	<u>4949</u>
B1020H18-A1 y	BACend		CATGATCTCAATAATTGCAACT	<u>4921</u>	GAAAGAAAACAGGAGAGTTGCAA	<u>4950</u>
B0756E08-A1 y	BACend		ATGGGTAATCACTATGCAIAGCA	<u>4922</u>	TTTAAAAATTCACCTTGCTATGC	<u>4951</u>
B0666F01-A1 y	BACend		GTGTCCTGGTGAAACGGCTCTGA	<u>4923</u>	AATCAGAGTTTCTCTCAGAGCC	<u>4952</u>
B0883G19-A1 y	BACend		ACATTTCCAGCTCTACATTTCTA	<u>4924</u>	CTGAGTTTCTCTCCTACAGAATGT	<u>4953</u>
B0923H14-A1 x	BACend		GATTAAGAGAGGGTAGGAGGGT	<u>4925</u>	ACCTTCCAACCATCACCCCTCCT	<u>4954</u>
B0781118-A1 x	BACend		GGATTAATAAGTACCACCCCTGT	<u>4926</u>	ATTTAACACAAAGGCGAGGGGT	<u>4955</u>
B0979G13-A1 x	BACend		GACATTTCCATGCAAAATGACAC	<u>4927</u>	CCCGCTTGCTTTTGGTGTCCAT	<u>4956</u>
B1020H18-A1 x	BACend		CATATGGCTAAGGCTCTATCTA	<u>4928</u>	AATCAGCAGGTACATAGATAGA	<u>4957</u>
B1029H23-A1 x	BACend		CAGCTAGGGGAAAGAGTGACAGG	<u>4929</u>	CGAAATGCCGAGCTGCCGTAC	<u>4958</u>
B1076C21-A1 x	BACend		CTAGAATTTCCATGTAGTAAGA	<u>4930</u>	ATACTTGCTCTTCTCTTACTA	<u>4959</u>
B1104N09-A1 x	BACend		CCTGCCTGATGAGCAAAAGAATA	<u>4931</u>	CACTGGGTACTTCTTATTCTTT	<u>4960</u>
B0663J16-A1 x	BACend		CAACCAACTATCTGCTGCCTTC	<u>4932</u>	TAGGTGAGTCTCTTTGAAGGCAG	<u>4961</u>

B0656F13-A1 x	BACend	GGTGTGAGAGAGTGGACTCTA	<u>4933</u>	TAATAATAAAATCCTTAGAGTCC	<u>4962</u>
B0883G19-A1 x	BACend	CATGGCACAGGTGATAGAGTGA	<u>4934</u>	ATAATCCAGGAAGATCACTCTA	<u>4963</u>
B0760A04-A2 x	BACend	GCTCTCATGATTTGGGCATGCT	<u>4935</u>	GTTCAAATCTTGCAAGCATGCC	<u>4964</u>
B0785D22-A1 x	BACend	GTGAACAGGCGTAACACTGTTAA	<u>4936</u>	ATGCCGTGCTGGTGTTTAACAGT	<u>4965</u>
B0723P10-A1 y	BACend	TGGAAGCCACTTAGAGGTTTGA	<u>4937</u>	AACAGTTTGGTACATGCAACCT	<u>4966</u>
B1095L07-A1 x	BACend	TCTAAAGATGGGGCTCACAGT	<u>4938</u>	ATGGCTTCAGTTTACTGTGAG	<u>4967</u>
B0997I04-A1 x	BACend	TACTTTACTCTGTTTCCGTAT	<u>4939</u>	AAGTGATATGAGACATACAGGA	<u>4968</u>
B0723P10-A1 x	BACend	AGGAAAGGGAAATAGAAAGGAA	<u>4940</u>	TAICTGCGTGGTGCTTCCCTTC	<u>4969</u>
B0997I04-A1 y	BACend	AGTGTAGTGGGAATGAGGAGT	<u>4941</u>	CTCCATTATCAGTCACTCCCTCA	<u>4970</u>
B0880L16-A2 x	BACend	GAAACCCACATCAGCACAAAGG	<u>4971</u>	TTTGCTGCTGGCTGGCCTTTGTG	<u>5000</u>
B0598O21-A2 x	BACend	CGCCGGAATTCATGACCTTTGA	<u>4972</u>	TTTGGCAGAATGTTTCAAGAGT	<u>5001</u>
B0768I12-A2 x	BACend	CACAAAGACAGAGACCCACAGCTC	<u>4973</u>	GCTGTGGGAAATGTGAGCTGTG	<u>5002</u>
B1056C02-A2 x	BACend	CCACACAGGAAAACTGCCATCT	<u>4974</u>	CCAATTCTCCTTTTCAGATGGCA	<u>5003</u>
B1056C02-A2 y	BACend	GAGACGTGAGTCAGGACAGGTG	<u>4975</u>	TGCCCAATCTGTACCACTGTCTC	<u>5004</u>
sts-AA017225	EST	GATGCCAGGAAGTACCTGTGTA	<u>4976</u>	GCAATCTCCAATCCTTACCAGG	<u>5005</u>
A004F14	EST	GGAACCCCGTGACTTGACCTTAG	<u>4977</u>	TGTCATCAGCACCCCTTAAGTCA	<u>5006</u>
SGC31333	EST	AGGTGTGATCTAGTCTCCGT	<u>4978</u>	GAGTGAAAGGTGGAAACCGGAGA	<u>5007</u>
WI-12422	EST	AACCAGACAGCATCTCTGAGAGA	<u>4979</u>	CACAGAGAGTGCAATTTTCTCTCA	<u>5008</u>
stSG21539	EST	ATGCATACAGCAGGCCATTGTG	<u>4980</u>	CAGCCCCCTATGACCACCAATGG	<u>5009</u>
WI-13120	EST	GGGAGCTACAGGTGATAGCTAT	<u>4981</u>	GGGGCCTATAGCTATCACCCTGTA	<u>5010</u>
stSG22703	EST	CACCAGAGACCAGAGACTCGAA	<u>4982</u>	ACCATGGACAGGCCCTTCGAGTC	<u>5011</u>
stSG36097	EST	TGAGCAGTCTGACCCTGCTTCTC	<u>4983</u>	AGCTGGAGGACCCTGGAGAAACA	<u>5012</u>
stSG9807	EST	CAGCCAGCTACTGAACCTTATG	<u>4984</u>	TGGCCCTAGGCACACATAAGGT	<u>5013</u>
stSG15434	EST	TACCACCACCCCTGCGCAGATGG	<u>4985</u>	GTANTCTGTGGCCGCCCATCTGC	<u>5014</u>
stSG30525	EST	GGCACACAGTCTGCAATGCTTG	<u>4986</u>	TAGGGACATCCCTCAAGCAAT	<u>5015</u>
A007A34	EST	TGTTCTGGCAGATTCCATCATC	<u>4987</u>	CTTATGTTGGGATGTGATGAG	<u>5016</u>
A006D44	EST	CAGGCTCATTCGAGGAGGAACA	<u>4988</u>	CGAAAGCTTGAATCTGTTCTCTC	<u>5017</u>
SGC30248	EST	GATGCAAGCAGCACAGAGCAGT	<u>4989</u>	CTCCTTCCACACAGCACTGCTCT	<u>5018</u>
sts-N20163	EST	TCTCTACCAAGCAATACTTCAC	<u>4990</u>	CTGAAATCGAGTGAAGTA	<u>5019</u>
Cda0af01	EST	AAAGGCCACACAGCCCAACAATC	<u>4991</u>	GGCCTGCAGTGGATGATTTGTGG	<u>5020</u>
Cda0ca07	EST	AAGTCTGACTTCAAAATCGGTAC	<u>4992</u>	TGCTTAAGCCCTCATGTACCAGAT	<u>5021</u>
stSG3292	EST	AAGTCTGACTTCAAAATCGGTAC	<u>4993</u>	TGCTTAAGCCCTCATGTACCAGAT	<u>5022</u>
SGC34088	EST	AAGTCAATTGCTCCCATCTGC	<u>4994</u>	CTTGTTGCTTGCTGGCAGATGG	<u>5023</u>
WI-12272	EST	GACTCATATGACAGACCTTGAA	<u>4995</u>	TGTCACACCTTTCTTCAAGGT	<u>5024</u>

sISG16387		EST		CATGACTCCAGACCCCTTAGA	<u>4996</u>	TGCCCAATTCTGTCTAAGG	<u>5025</u>
SGC31722		EST		CAACGGAGAAAGCCCCAGATAC	<u>4997</u>	TTGTTACTGTACGTGTATCTGG	<u>5026</u>
WI-15018		EST		AGTGACAATTAGAGCTCTGGGG	<u>4998</u>	GCTCCTTCAATTCTCCCCAGAG	<u>5027</u>
WI-18492		EST		TGCTTGGCCAAACAGACTTCT	<u>4999</u>	TGATGAGACTGCAGAGGAAGTC	<u>5028</u>
sISG9546		EST		ACCTGAGAGCAGGGAGATTCCA	<u>5029</u>	TAACTCCTAGCAGCTGGAATCT	<u>5058</u>
A006O16		EST		CCCGAGGCTTCTCTGAACACTA	<u>5030</u>	CTCACAGCGCTTCTAGTGTTT	<u>5059</u>
H64839		EST		AATCTGAGGCACACAGGAGAGT	<u>5031</u>	ACTGAGCTCCTTTCACTCTCCT	<u>5060</u>
sISG3357		EST		GCCTTGCTAACTGTACCATAGT	<u>5032</u>	CACCTGCAGGAATACTATGGT	<u>5061</u>
sISG30906		EST		TCTAAGGTTCCGGATGGACGTG	<u>5033</u>	TGTCCCGCCAAATTACCGTCCA	<u>5062</u>
sISG26056		EST		GAGTTACAGGAAGTGGTTCCCC	<u>5034</u>	CTGCCGTGTCTGTACGGGGAACC	<u>5063</u>
SGC30786		EST		ACAGCTCTCCTTCCTTAATGCC	<u>5035</u>	CACCCTTATCTCTGGGCATTAA	<u>5064</u>
sIS-N59820		EST		AGACTGCATCCTTCGAACAACAGG	<u>5036</u>	ACTGGGAATCTAGCGCCTGTGT	<u>5065</u>
sISG42115		EST		TTCTCGAGGGTCTCTGCTTCACT	<u>5037</u>	AGTTCTCTCGGAGTTAGTGAAGC	<u>5066</u>
FB9F8		EST		GAAAAACCCCGCACCCCTGACACAAAC	<u>5038</u>	CGTCCAGAAAAACGTAGGTTGTGTC	<u>5067</u>
AA252357		EST		CAGCACATCGAGTCCCTCAAAATCCG	<u>5039</u>	CCAGACTTTCCTCACTCGGATTTG	<u>5068</u>
sISG4720		EST		TCGAGAAAGGCTGTTCCTACAAGG	<u>5040</u>	TAACTCAGGACCTTCCCTTGTAG	<u>5069</u>
sIS-AA001424		EST		AAGCTGCTCTTCTCAGCTACTCTG	<u>5041</u>	TTTCAGGGTTCTGGGTCAAGTAG	<u>5070</u>
sISG31443		EST		CAAAAGCACTGGACTGAGAGAATTTC	<u>5042</u>	GGTGGATACAGTGTGTGAATTCTC	<u>5071</u>
WI-6385	D12S1405	EST		TAAAGGCAAAAGGCCACACAGCCCA	<u>5043</u>	CTGCAGTGGATGATTGTGGGCTGT	<u>5072</u>
A008Y05		EST		TAAAGATAAAGCGGTGGCTTTTGAC	<u>5044</u>	AACTCTGGCAGACACTGTCAAAAGC	<u>5073</u>
R50113		EST		TCATACCAAAGTGTGGCTGTAAAG	<u>5045</u>	CCAGTTTCTCCACATCCTTAGCAG	<u>5074</u>
sIS-H94865		EST		CTCTAAGAACCCAGACCCCTCAGTTG	<u>5046</u>	CTCATTTCCCTTACTGGCAACTGAG	<u>5075</u>
A006R19		EST		GGTTTGAACAGTGGGAGATACCAG	<u>5047</u>	TTTTCTCCTCCACCTCTGGTATC	<u>5076</u>
SGC34278		EST		CAAAACACAAGAGGTCCTCTTGCTG	<u>5048</u>	ACAGTCCATGGAAGGCAGCAAGA	<u>5077</u>
A004B47		EST		GTGCCCTGTGAATTGGCCTTTCT	<u>5049</u>	GCTGGAAGCAGAAAGGAAGAAAGGC	<u>5078</u>
sISG40199		EST		GGAAAGGCTGTCTTCTTTCTACCAC	<u>5050</u>	TGACACCTGCCCTCATGGTGTAGA	<u>5079</u>
sISG8935		EST		CAAAACACAAGAGGTCCTCTTGCTG	<u>5051</u>	ACAGTCCATGGAAGGCAGCAAGA	<u>5080</u>
sISG4731		EST		GCAATGTGTTGTTTCTGTCTGGGAT	<u>5052</u>	AGCAGACAAGATCTAGATCCAGA	<u>5081</u>
sISG8142		EST		GTGCCCTGTGAATTGGCCTTTCT	<u>5053</u>	GCTGGAAGCAGAAAGGAAGAAAGGC	<u>5082</u>
A005X42		EST		GCATGTGTTGTTTCTGTCTGGGAT	<u>5054</u>	AGCAGACAAGATCTAGATCCAGA	<u>5083</u>
CDA18G06	D12S1205E	EST		ACAGACTACAAACGTCAATGAAGCC	<u>5055</u>	TCCGACAATGCCAGGAGGCTTCAT	<u>5084</u>
STSG40222		EST		TCTTCTCTCTACCTGCAGACCATG	<u>5056</u>	TGCCCACATGGAGAAACATGTCT	<u>5085</u>
sIS-R55615		EST		GCTAGTGAACGGATAACCTGAAG	<u>5057</u>	CTTCCTGTGGTAGTGTCTTTCAAG	<u>5086</u>
sIS-R02295		EST		CTCAATCCACATGACAACGCTTTG	<u>5087</u>	ACCTAGTATCCTACCTCAAAAGCGT	<u>5114</u>

sis-R81342	EST		GGCAAAAGGGAAAAACCATGTATG	<u>5088</u>	TCACCTCCCTTACAGTCATACATG	<u>5115</u>
sis-H65839	EST		AATAGATTGATTGCCGTCCTCAAC	<u>5089</u>	AAATATGTGCTAACTTGTTGAGGA	<u>5116</u>
sisG52716	EST		AGATGGGGAGACAAACGGTAAAC	<u>5090</u>	CGGAAAGGAAACATCTGTTTACCG	<u>5117</u>
sisG54813	EST	highly similar to 22 kd peroxisomal membrane protein	TTTGTGTCAGCTGTCCAACCA	<u>5091</u>	TGCAGTAATGGATGGGTGTTGGA	<u>5118</u>
sisG50504	EST		CCGTATTACCCAGACTACACACTG	<u>5092</u>	CACCAATGGCATAGCACAGTGTGT	<u>5119</u>
sisG48386	EST		CCAGCAGCAGGATATTGTGTACGT	<u>5093</u>	GTTTACAGCCTACAGGACGTACAC	<u>5120</u>
sisG54842	EST		TTCTTCTCAGGTCGCCGCTCAAG	<u>5094</u>	TCACGGCCTACGAGATCTTTGAGC	<u>5121</u>
sisG53600	EST	Highly similar to peptide transporter PTR2	AACGTGGATGCCCACTAACACGTTG	<u>5095</u>	AAGTCTGGGGAACTCACGTGTT	<u>5122</u>
sisG53541	EST	Homo sapiens hiwi mRNA, partial cds	AACCCCACTATGTTGTAGTGAG	<u>5096</u>	GGCGTAAAGTAGGATGCTCACTAC	<u>5123</u>
sisG53307	EST		GAGGCTAGGCTGAATATAACCCAGG	<u>5097</u>	CACTGCCAGTCAGCAACCTGGTTA	<u>5124</u>
sisG63473	EST		CCACTGGCTGCATTTCCAGCTTT	<u>5098</u>	CACCAGGTACTAGAGAAAAAGCTGG	<u>5125</u>
sisG54325	EST		CGGCACAAGCAGATTTCAGATCAG	<u>5099</u>	CTGGGGGAAATGCTGACTGATCTG	<u>5126</u>
sisG52343	EST		AACGTGAGTCAGGTGATCACCGAAG	<u>5100</u>	CCAGTGAATAAGCCCCCTTCGTGA	<u>5127</u>
WIAF-856	EST		AAGTCAATTGCTCCCCATCTGCCA	<u>5101</u>	TCTACTTGTTGTTGTTGCTGGCAGAT	<u>5128</u>
sisG47723	EST		CTGAGTTCCCTAGCAGCTTCGTA	<u>5102</u>	TCTTCAAAAGGACCTCCTACGGAAAG	<u>5129</u>
sisG60065	EST		GGAGGTGAATAAGCTGATCCTGCA	<u>5103</u>	GCTGGGTAACTAGAAAGTGCAGGAT	<u>5130</u>
sisG46424	EST		GGACACATCTGTTCCATCTTCACC	<u>5104</u>	CCCATGAGTTGTTAGTGTGAAGA	<u>5131</u>
sis-U79526	Gene	DEZ	TGATCCTCACTGTGAAACCCCT	<u>5105</u>	GAGAGAGTCCATTGAGGGGTTT	<u>5132</u>
SGC31491	Gene	NOS1	AGAGCGGCTCTTTTAATGAGGG	<u>5106</u>	GGGAGACGTCGCCAACCCCTCATTT	<u>5133</u>
sisG1936	Gene	CLA-1	TCAGTCCATAGGATGATGTGAG	<u>5107</u>	TCCTCCAGCCTAAACTGACATC	<u>5134</u>
sis-W31616	Gene	UBA52	CCCAGCAAAAGATCAACCTCTGC	<u>5108</u>	ATCCCTCCTGATCAGCAGAGAGT	<u>5135</u>
ZNF10	Gene	KOX 1	ATGTGGGAAGCCTTTGGTAGT	<u>5109</u>	GTAAGGTTTGAGCCACTACCAA	<u>5136</u>
ZNF26	Gene	KOX20	GTGAATGTGAAAAAGCCTTCAC	<u>5110</u>	GAGATGACTTCTGAGTGAAGGC	<u>5137</u>
WI-6921	Gene	RNP24	GTTGCAAGTGTCTCACCCAAAG	<u>5111</u>	AACCAIACCTTCACCTTGGGTG	<u>5138</u>
sis-D60472	Gene	SMRT	GAACGACGTGTGTAATGACAG	<u>5112</u>	AGGGTGGTGATATTCTGTCAATT	<u>5139</u>
WI-16177	Gene	RAN	CCTTCAGGCATCCACACAGATGA	<u>5113</u>	CGGAACATGTGCCCTTCATCTGT	<u>5140</u>
sisG1702	Gene	CAGH32	TCAGGCACCAAAATCTGAACAAGGG	<u>5141</u>	GAAAGTTGGATCCCAAGCCCTTGTT	<u>5170</u>
IB2452	Gene	ULK1	GCCATCAAGGTGATGAGGAAGAAG	<u>5142</u>	AAGAAAAATCCCCGTGACTTCTCC	<u>5171</u>
sisG39493	Gene	CAGH32	GTGCTGAATCTCTTGCGTGACATG	<u>5143</u>	TAGTGAACCTTGGGACCATGTACAC	<u>5172</u>
A002A44	Gene	CAGH32	TGGTCTCTGCTTCACCTGGCAGAA	<u>5144</u>	GGATAAGCTTGTGTGTTCTGCCA	<u>5173</u>
sisG27206	Gene	GCP170	GAGCACATCTGGCCTGGCCAGT	<u>5145</u>	TGAGGTTCTGAGTCACCTGGCCA	<u>5174</u>
CDA1JF08	Gene	GCP170	AGTGAGCTCAGAACACCTCACACC	<u>5146</u>	AGTTGAGTGACGCTGTGTGTGAG	<u>5175</u>

R39599		Gene	GCP170	ACTTCTGCAGTCATCGAGAAGTCC	<u>5147</u>	CCCACAAAAGATCCCAAGCACTTCT	<u>5176</u>
sISG31494		Gene	ZNF140	TCTCCAGTATGAGTCTCTGTGT	<u>5148</u>	GCTTTTCCCTGGTGTACACCAGA	<u>5177</u>
TH_a		Gene	MUC8	ATCCACCGCTAGAAACCCACTC	<u>5149</u>	GACCATCAACTGATGAGTGGGT	<u>5178</u>
SGC31491_a		Gene	NOS1	CCTAGTAGCTTTCTCCCAAG	<u>5150</u>	ATTGAAAGAAAGCCTTTGGGA	<u>5179</u>
sis-X89576		Gene	MMP17	AGAGGAGCTGTCTAAGGCCATC	<u>5151</u>	TGCTGCATGGCTGTGATGGCCT	<u>5180</u>
sISG43910		Gene	SFRS8	caglacaigtltaccacagac	<u>5152</u>	tgcacataigtcacagacacc	<u>5181</u>
P699K7.17	D12S2479	Genomic		AGAAAGCCTCTCTTCCCTCTCTC	<u>5153</u>	GTCACATTTTGGGCTGAGAGAGG	<u>5182</u>
P493P14/T7	D12S2451	Genomic		TCTCAGGAACCAAGAGTCCATAG	<u>5154</u>	CAGTTAGATAAAAGCTATGGAC	<u>5183</u>
P313C9/SP6	D12S2447	Genomic		CAGCTCAGGAAGTTCACCAGGC	<u>5155</u>	AGGACCCAGTTGAAGCCTGGTG	<u>5184</u>
WI-5824	D12S2002	Genomic		CATTTAACCTGCCCGCTGTCA	<u>5156</u>	CAGGATTTGTGTGTGACCAGG	<u>5185</u>
WI-10803	D12S1944	Genomic		CTGGATTTCCAGAGACTGACCT	<u>5157</u>	TCAGGCCAATAGAGAGGTCAGT	<u>5186</u>
WI-2002	D12S1084	Genomic		ACAACAGAAAGTTGTAGTGAAG	<u>5158</u>	CTGTTCAACAGTGCCTTCACTG	<u>5187</u>
WI-3045	d12S1420	Genomic		CTTAAGCGAGCAACCTGATAACCC	<u>5159</u>	TCCTAATCTGGCAGGTGGGTATC	<u>5188</u>
WI-3549	D12S1998	Genomic		GAGAAATCAGCTGCCATGTTGTAG	<u>5160</u>	GGACTCTTTGAGCATCTCACAAC	<u>5189</u>
WI-6077	D12S1322	Genomic		AGCAGCACIAGGCATGGCTGTT	<u>5161</u>	ATAAGAGCTGAGATAACAGCCA	<u>5190</u>
SHGC-12243	D12S1845	Genomic		CAAGCTTCCCCTCTTCCCATTTGT	<u>5162</u>	TTCCGGCGTTGTAGTTACAATGGG	<u>5191</u>
SHGC-13782	D12S1851	Genomic		AGTCAGGTACAGGGTTCGACAAC	<u>5163</u>	CACCTTGTTGCTCTCTGTTGTAG	<u>5192</u>
SHGC-14238_a	D12S1853	Genomic		CAAGTGTCCCACTTTTCTGCA	<u>5164</u>	CCGCTCACTCACTCTGCAGGAA	<u>5193</u>
WI-3549_a	D12S1998	Genomic		CCATGTTGTGAGGATGCTCAAA	<u>5165</u>	ACCTTTTAAAGACTCTTTGAGCA	<u>5194</u>
AFMb337xc1	D12S1675	MSAT		GATCTGCAGCATTGAGGGAGCA	<u>5166</u>	GTCCTAAGGCACATTGCTCCCT	<u>5195</u>
AFMa197zd9	D12S1609	MSAT		GGGGATTTAGTAGNTCAATGTA	<u>5167</u>	GTCAICGGGTGACATACATTGA	<u>5196</u>
AFMb350zb5	D12S1679	MSAT		GTTTGTAGGCTTCTTGCCCTGTG	<u>5168</u>	CCCTCTACCAATTCACAGAGCA	<u>5197</u>
UT7009	D12S834	MSAT		GTCCAAGAGTGGGCAAGTTGACC	<u>5169</u>	ATTGATAGGCATAGGTCAACT	<u>5198</u>
AFMb301we5	D12S1659	MSAT		TCTAACTTTGCTTGCCCTGCTT	<u>5199</u>	CACGTGTGCTTTCAGAAAGCAGGC	<u>5214</u>
AFMa064xg9	D12S1714	MSAT		GTTCGAGATCCACAGGTGTCTA	<u>5200</u>	TGTAGCATATGATGTAGACACC	<u>5215</u>
CHLC ATA19A06	D12S2069	MSAT		TGTTGCCCTAGGCTGTGCTTCAA	<u>5201</u>	CTTGAGTCCAAGAGTTCAAGAC	<u>5216</u>
ATA29A06	D12S1045	MSAT		GACCAGCCTIAGGCACATAGTGA	<u>5202</u>	TTAGAGATGGGCTCTCACTATG	<u>5217</u>
AFM210zd6	D12S97	MSAT		AATTGTTCTCATGGGCTCGAA	<u>5203</u>	CCTTCACTGAGGAGTTGAGCC	<u>5218</u>
AFM295ye9	D12S343	MSAT		TACTGCCACTCTCAGAAATATC	<u>5204</u>	GATCTGGAAGGTGGATAATTCT	<u>5219</u>
509/510	D12S63	MSAT		GTGGTTGGGTTAACAAAGAATG	<u>5205</u>	GAGAAAGCTGCAACGCATTCTTT	<u>5220</u>
AFMa275xb9	D12S1628	MSAT		AAGGTAGAGCTTGGCAACAGGA	<u>5206</u>	AGCCCCGCTGGACCTCTGTTG	<u>5221</u>
AFMb002vd5	D12S1638	MSAT		TGCCAGGAGTTTAAAGTTGCTT	<u>5207</u>	GAAITGGCATTGTGTAACCAACT	<u>5222</u>
GATA13D05	D12S392	MSAT		GTAITGATAGCAGACGATAGAG	<u>5208</u>	TCTATCTGTCAATCCCTCTATCG	<u>5223</u>
12QTEL82	D12S2342	MSAT		TACATTCACACAGCAGTGCACAAAG	<u>5209</u>	TGGAGAAATTGGAAGCCTTGTGCA	<u>5224</u>

12QTEL87	D12S2343	MSAT		TTGTTAGGCTTCTGGGTTGGGTAC	<u>5210</u>	ACAGGCATTAGCCCCCTGTACCCAA	<u>5225</u>
AFMa082ze9_a	D12S1723	MSAT		CTCCGTCATGAATGTCAGTAG	<u>5211</u>	TCTGCAGTGGTTCCCTACTGAC	<u>5226</u>
AFM156xc5_a	D12S1599	MSAT		TGGGAAGAGTTGCCCTCCAGGAA	<u>5212</u>	CCCTTCTCAGTCCCTTTCCTGGA	<u>5227</u>
AFMa123xe1	D12S367	MSAT		CTGTATTAAATGAGTCTGGGT	<u>5213</u>	GGGTTAATAACAGTTAACCCAGA	<u>5228</u>

Please replace lines 7-8 at page 144 with the following rewritten lines:

-- SEQ ID NO: 5229) and pBAC 3'-1 (CGA CAT TTA GGT GAC ACT; SEQ ID NO: 5230). --

Please replace lines 30-31 at page 145 with the following rewritten lines:

-- adapters (5' GTCTTCACCCACGGGG (SEQ ID NO: 5231) and 5' GTGGTGAAGAC (SEQ ID NO: 5232) in 100-1000 fold molar excess. These --

Please replace Table 5 on page 162 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 5: PAIRED LINKERS

<u>Paired linkers</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Cell/Tissue Type</u>
OLIGO 3	5'CTC GAG AAT TCT GGA TCC TC3'	<u>5233</u>	Th2/unstimulated (dT+rp)
OLIGO 4	5'TTG AGG ATC CAG AAT TCT CGA G3'	<u>5234</u>	Th0/stimulated/anti CD3 (dT+rp)
			Pulmonary artery endothelium cells (dT+rp)
			Lung microvascular
			Endothelial cells (dT+rp)
			Bronchial epithelium cells (dT+rp)
OLIGO 5	5'TGT ATG CGA ATT CGC TGC GCG3'	<u>5235</u>	Normal Lung (dT+rp)
OLIGO 6	5'TTC GCG CAG CGA ATT CGC ATA CA3'	<u>5236</u>	Athmatic lung (dT+rp)
			Th2/stimulated/TPA (dT+rp)
			Bronchial smooth muscle cells (dT+rp)
OLIGO 9	5'CCT ACG GAA TTC TCA CTC AGC3'	<u>5237</u>	Brain (dT+rp)
OLIGO 10	5'TTG CTG AGT GAG AAT TCC GTA GGG3'	<u>5238</u>	Th0/unstimulated (dT+rp)
			Pulmonary artery smooth muscle cells (dT+rp)
OLIGO 11	5'GAA TCC GAA TTC CTG GTC AGC3'	<u>5239</u>	Lung fibroblasts (dT+rp)
OLIGO 12	5'TTG CTG ACC AGG AAT TCG GAT TC3'	<u>5240</u>	Th0/stimulated/ TPA (dT+rp)
			Small airway epithelium cells (dT+rp)

Please replace Table 7 on page 165 with the following table:

TABLE 7: MODIFIED OLIGONUCLEOTIDES

Modified	SEQ	
<u>Oligonucleotides</u>	<u>ID NO</u>	<u>Sequence</u>
OLIGO 3	<u>5241</u>	5' CUA CUA CUA CTC GAG AAT TCT GGA TCC TC 3'
OLIGO 5	<u>5242</u>	5' CUA CUA CUACUATGT ATG CGA ATT CGC TGC GCG 3'
OLIGO 9	<u>5243</u>	5' CUA CUA CUA CUA CCT ACG GAA TTC TCA CTC AGC 3'
OLIGO 11	<u>5244</u>	5' CUA CUA CUA CUA GAA TCC GAA TTC CTG GTC AGC 3'

Please replace Table 8 on pages 170-176 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 8: SSCP PRIMERS

Primers used in SSCP experiments					
Gene	Exon	SSCP Assay	SEQ ID NO:	Forward Sequence	SEQ ID NO: Reverse Sequence
454	A	55_454_A_F_56_454_A_R	5245	TGGCCCTGTACGGAAGAGTA	5271 CTGCAGAGATCTGGGTCCTC
454	B	57_454_B_F_58_454_B_R	5246	TTGATGCTTTCCCATGTCTG	5272 GGAGAATGCTACGAGGTGCT
454	C	59_454_C_F_60_454_C_R	5247	TCAAGAGCCTTGCAATTTCT	5273 GTCCGATTTCTGCTTCTTC
454	D	61_454_D_F_62_454_D_R	5248	TCCCACCTCTGTCAATCCTTC	5274 GAGGCTGAAGACCTGACCCTG
454	E	63_454_E_F_64_454_E_R	5249	CCTCTCCGCAAGTTCTTTTAC	5275 GAGGGCCACTGTGTCTGTCT
454	F	65_454_F_F_66_454_F_R	5250	GTATCCCAAGACCAAGCCA	5276 AACTAAGACAGCCAGGCAGC
454	G	67_454_G_F_68_454_G_R	5251	ATGGAACCTCTCCACACACAC	5277 TCCAGTGTACAAAGCACCA
454	H	69_454_H_F_70_454_H_R	5252	CTGGCTATGCAAGGAGATGT	5278 GTGAGTTGACCTGGGCCT
454	K	71_454_K_F_72_454_K_R	5253	CCAGAACCCAGCACTTTCA	5279 AGGCTGAGACCAAAACCCTT
454	L	73_454_L_F_74_454_L_R	5254	AACCAACAATTGCACGTTGA	5280 TGTGATGAGGAAGTCGATG
454	M	75_454_M_F_76_454_M_R	5255	CAGCGCTGTCTGCATTCT	5281 GGAATCTCTCCGTGTCTTGG
454	N	77_454_N_F_78_454_N_R	5256	TGATAATTCTGTACAAAATGGGTAA	5282 CTTTGTAAATCCATCAGTTTGG
454	O1	79_454_O_F_80_454_O_R	5257	CCTAGAACCTGAGGGCTGTGTC	5283 CTGTGGCTCTCAGGGAGTTG
454	O2	81_454_O_F_82_454_O_R	5258	GGTGCCAGTGTGGAAGATG	5284 AGGTGGCGTAGCACCTGTAG
454	O3	83_454_O_F_84_454_O_R	5259	CACCACCTCAGAGCTGTTCA	5285 ACTGCCCTTCACCTCTTTGGA
454	O4	85_454_O_F_86_454_O_R	5260	CCAGGACATGGCTGACTTTG	5286 ACAGACAGGATTTGCGCCTTG
454	AA	1959_454_AA_F_1960_454_AA_R	5261	GAAATATTCCAATTTTGCCCTGG	5287 CCGAGGAAAGTGAGTTGAG
454	AA	1961_454_AA_F_1962_454_AA_R	5262	CCTGTTTTGCTTTGAGTCCA	5288 TACTCTCCACCCCTCCTCTGC
454	AA	1963_454_AA_F_1964_454_AA_R	5263	CCTGGTGATCTTTGGCTGAT	5289 ACAACCCTTTATTACAGCCCC
454	AA	1965_454_AA_F_1966_454_AA_R	5264	GGGAGATCTTCATTTACCCA	5290 GTGTTCAGAGGATGGGCATT
454	AA	1967_454_AA_F_1968_454_AA_R	5265	GGGGAAGAGGAGAAATTTCTAAA	5291 CCTCCAGTAACCTGCMAAA
454	AA	1969_454_AA_F_1970_454_AA_R	5266	GCAGTCAATTGGAGGAGCTTG	5292 GGAAGAGATGATCACGTTGAA
757	A	1750_757_A_F_1751_757_A_R	5267	GAGCAGGGGTGAGAGAGCC	5293 CAGGTTGGGATACGAGTCA
757	A	1752_757_A_F_1753_757_A_R	5268	GCAAGGACATCGGCTACAA	5294 ATAATCGGGGAGCACCTTGAG
757	A	1778_757_A_F_1779_757_A_R	5269	TGCACCGAGCAGGCTCTAC	5295 GTCTTCAGCGGGTGCTC
757	A	1780_757_A_F_1781_757_A_R	5270	AACTACCTGTGATGAGGC	5296 GAAGGTGAGCAGCGGTGAAG
757	A	1758_757_A_F_1759_757_A_R	5297	CGTGCTCAACCTTCTCTATC	5330 GTGAGGACCACCCACCAC
757	A	1760_757_A_F_1761_757_A_R	5298	CTGTGGTGGGTGCTCTC	5331 GTAGCAGGCCAGGGGAAT
757	A	1782_757_A_F_1783_757_A_R	5299	TCTGCTACGTGGGCAGCAT	5332 CCATGTTGAGGCGTTCGTAA
757	A	1784_757_A_F_1785_757_A_R	5300	CTCTGTGCTGTACACCGTGC	5333 GGTTCCTCCGGCTCTTCTT

757	A	1786_757_A_F_1787_757_A_R	5301	CCTCCAAGACTCTGCAGTCC	5334	CACAACCAAGAAAGCACCA
757	A	1788_757_A_F_1789_757_A_R	5302	AAATATGAGATCCCTGCCA	5335	CTTCGCTGAAAAACCAAAAC
757	A	1768_757_A_F_1769_757_A_R	5303	TGAAATTGAGGATGCTGTGA	5336	TTGCAAAAGCAGTTATCTGTCC
757	A	1770_757_A_F_1771_757_A_R	5304	TTGAGTTGGCTTTGCTACCC	5337	TGTGAGGTTTGATGGAGGTTT
757	A	1772_757_A_F_1773_757_A_R	5305	CTGCAAGACAGAAACCTCCA	5338	TCCACAAATCAGTCCAAACG
757	A	1774_757_A_F_1775_757_A_R	5306	TAATGGAACCAAGCCAATG	5339	CAATATATACACACGAGAAACC
757	A	1776_757_A_F_1777_757_A_R	5307	TGCCAGGAAGAGTGGTTTC	5340	GCTAGGAAGCACACACCCAGAG
561	A	1530_561_A_F_1531_561_A_R	5308	AGGGTATAGGATGCACGCC	5341	CTCCACCACACACAGGAT
561	B	937_561_B_F_938_561_B_R	5309	ACACACATTTCACCACCAA	5342	CATGAACGTGGGAAAGGCT
561	B	939_561_B_F_940_561_B_R	5310	CCGGACTCAAGTGAGCAGT	5343	ATTTCACCTGTGCACACCCCT
561	C	941_561_C_F_942_561_C_R	5311	CATGACCACAGTGTCTTGAC	5344	AICTTGGCTIACCGGATCT
561	C	943_561_C_F_944_561_C_R	5312	GTCAGGAGAGCGCTATTGGA	5345	AACAGGACAAACTGGCCAAC
561	D	945_561_D_F_946_561_D_R	5313	CCTCCAGCTTCAATAACCCA	5346	AAATCCCACTTCTCCTCGT
561	E	947_561_E_F_948_561_E_R	5314	TGTGTCTCCAGAGCCTCTAA	5347	GGGAGCCCTGCCCTATCTATC
561	F	949_561_F_F_950_561_F_R	5315	CTGTGTTGGCTGGTGATAA	5348	GGCACTGTTGTGGTGATG
561	F	951_561_F_F_952_561_F_R	5316	GAGAGCACATCCTGGACCTC	5349	TTCATGCGTGTCTCCTTGTC
561	F	953_561_F_F_954_561_F_R	5317	GCCACCAGGATGGGGAAC	5350	TCTGCGTGATGTTGTCAC
561	F	955_561_F_F_956_561_F_R	5318	GTGGCAAGGACGTGTG	5351	CTCCCTTTGCTCCAGCGG
561	F	957_561_F_F_958_561_F_R	5319	CACGTGATCTTCTCAACGA	5352	GGAAGGACACAGGGCTCAC
561	G	1532_561_G_F_1533_561_G_R	5320	ACCGAATGATCTCGTTCCA	5353	AAAACTCACCCCTCTGCCCTT
561	G	1534_561_G_F_1535_561_G_R	5321	CACCCCCACAAGATGTTACC	5354	AGTGATCAGGGCTGGAAGAG
561	H	961_561_H_F_962_561_H_R	5322	GGCTCCCAATTGCAGGAC	5355	TGATTGGGGTGCAGGTCTC
561	H	963_561_H_F_964_561_H_R	5323	ACTCTGCAGTTGCTGCCGT	5356	CTGTGGCTGTGGCAGGAT
561	H	1536_561_H_F_1537_561_H_R	5324	CACGCCAGGATGGATGAG	5357	GACTGAGGAGCCACCCGAG
561	I	967_561_I_F_968_561_I_R	5325	GTAGCTGAAGGTGGCCCTG	5358	CCACCAGGAGGATGTGT
561	J	969_561_J_F_970_561_J_R	5326	TGTAGGATGCGGAGGAG	5359	AGCTACTCTGGGGACGGAG
561	K	971_561_K_F_972_561_K_R	5327	ATGCTGGCGAGACTTACGAC	5360	TTTGCTTAGCGGAAATGCT
561	L	973_561_L_F_974_561_L_R	5328	CACGCTCCTCAGTTAGGCTC	5361	CACCTTGATGATCTGGCCCTT
561	L	975_561_L_F_976_561_L_R	5329	AGACCGCCTTCTCCAGACT	5362	GTCGATACCCCTGTTGCCAGT
561	M	977_561_M_F_978_561_M_R	5363	CTGAACCAATCAATTACAGTCT	5366	GATAAAATGCACAGGGGAAGTCT
561	N	979_561_N_F_980_561_N_R	5364	AGGGGAACACCGCTAAGTTT	5397	GTTGGTGTACCACGAGGGAAG
561	O	1538_561_O_F_1539_561_O_R	5365	TTCTCAATAGTAAGGGAAGCA	5398	ATGACGTTTATGCCCCAATTT
561	P	983_561_P_F_984_561_P_R	5366	TCCTTTAGCCAAAGCAAGATG	5399	ATATGGCAGAAACGGGACAGA
561	Q	1248_561_Q_F_1249_561_Q_R	5367	CCAAGGGCTTCTCAAGCATA	5400	ACACTGGCCCGGTTAAGGTA
561	X	1744_561_X_F_1745_561_X_R	5368	GCCCCTAAGTATACAGAGGAA	5401	AAGGAGGACAGACAAAGCAAA
561	Y	1746_561_Y_F_1747_561_Y_R	5369	GGAGCTCCTAACCCACTGCAC	5402	CTTCCAGTTGTTCTCCTCCT
561	Z	1748_561_Z_F_1749_561_Z_R	5370	AGAGGAAGCAACGGATACCA	5403	TCACACCGACCTCACAAAGA
561	R	1957_561_R_F_1958_561_R_R	5371	ACCTGCCACGATAGCACACAG	5404	ATAGGTGAGGAGGAACGTGGC

214	B	192_214_B_F_193_214_B_R	5372	CACGTGTTAAACCGCTGG	5405	GTTGGATTACAGGCACGAG
214	B	194_214_B_F_195_214_B_R	5373	CAGAAACAACCCACATGACC	5406	ACTACAGGTTTGACCACCA
214	A	196_214_A_F_197_214_A_R	5374	GCCCTTAGGAGAGCAGC	5407	CCACATCGTGCCTTTGTGA
214	C	626_214_C_F_627_214_C_R	5375	ATGCTCTCCTGATGGCTCCT	5408	AGGGAATGCAGGTGCAAG
214	C	628_214_C_F_629_214_C_R	5376	ACTGGGAAAGGAAGGCTCT	5409	CATACCTTGAGTGCACACCG
214	AA	1607_214_AA_F_1608_214_AA_R	5377	AGACAGTGTGTTCCCGGAG	5410	TCACTGCTCACCCACGTTAG
214	E	1609_214_E_F_1610_214_E_R	5378	ATATGTTTGCTGGCTTTGGG	5411	GAAAGAGTGAGCCGGTAACA
214	E	1611_214_E_F_1612_214_E_R	5379	CTGCTTCAAGATGCCAGTGA	5412	AACAAACGCCCTGGGTTGAG
214	E	1613_214_E_F_1614_214_E_R	5380	CCGTCCCAGGATACCTTTTC	5413	CCCAGGCTGTGTCTCCTTA
214	E	1615_214_E_F_1616_214_E_R	5381	ACACCCATCACCTTACATGG	5414	AATGAACGTGGTGACTACAGC
214	E	1617_214_E_F_1618_214_E_R	5382	TATCTGACCGTGGTGTGC	5415	AGCAGAGTGAACAGTGGCTG
214	AA	1599_214_AA_F_1600_214_AA_R	5383	CGGGCGTGTATATCTCTTCA	5416	TTGCTGTGTGATCATGTGC
214	AA	1601_214_AA_F_1602_214_AA_R	5384	TGTACGAACAGTCCAGACGAG	5417	GCCATGTTGTTAAATTAGGC
214	AA	1603_214_AA_F_1604_214_AA_R	5385	CGACATGATCACAAAGCGAAA	5418	TTTGGTCTGCTTCAGTGGTG
214	AA	1605_214_AA_F_1606_214_AA_R	5386	CGAATAAAGCGCTCGAGAAG	5419	CAGGGTCCTCTTCAGAGTCG
224	W	133_224_W_F_134_224_W_R	5387	CACCTGTCACCTGCCTTGTA	5420	GGGACCCACCTTGCTGAG
224	BB	1432_224_BB_F_1433_224_BB_R	5388	CCCAGCCCCCTTCTCACTG	5421	GGAAAAAGGACCTGGGAAGT
224	C	1434_224_C_F_1435_224_C_R	5389	CAGCAAGTCCCTCCTGATGT	5422	TTTAGCTTCCCTCCCTCAG
224	D	1436_224_D_F_1437_224_D_R	5390	GCAGATCCCAAGGAAGAACAA	5423	AGCTGCCACCTCTCATCTA
224	J	1438_224_J_F_1439_224_J_R	5391	TGTGGGGTACAGTGGCATTGA	5424	GCAAAACCCACTCACCCCTCT
224	L	1440_224_L_F_1441_224_L_R	5392	ATCCAGAGATACCCACGCT	5425	CAAAAGTGGTTTCTGGCAGT
224	Y	1442_224_Y_F_1443_224_Y_R	5393	GCCTGTGGGTAITTTGCACT	5426	ACCTACCCCAACTTGTGACG
224	Z	1444_224_Z_F_1445_224_Z_R	5394	TTGATTGGATTTGAGCTCTGC	5427	CCGTGGAGAGACACCTTCAC
224	S	131_224_S_F_132_224_S_R	5395	TTGGCAGACAGAAGAGGAGG	5428	TTTCTGTAGGTCATGAG
422	C	1859_422_C_F_1860_422_C_R	5429	TTATCTGGGCGAGGTTGTGT	5462	CCCATTCAGAGGAGTGAGA
422	D	1861_422_D_F_1862_422_D_R	5430	CTGGCAGACCCGATTTGAAC	5463	GGCAGGCACTCCAAATTTTC
422	E	1863_422_E_F_1864_422_E_R	5431	GTGAGGGCTGACCTATTGCT	5464	CGGCCCTACTGAGAACCAACT
422	F	1865_422_F_F_1866_422_F_R	5432	TTCTTCTTGCCCCAGATTGT	5465	TGAGATGAGGCAGATAGAGGTG
422	F	1867_422_F_F_1868_422_F_R	5433	AAGGCACACAAGAACCTGGA	5466	AGGTGGCATCACTGCACCTC
436	A	1549_436_A_F_1550_436_A_R	5434	CCTAGAGGGTCAATCGTTCCC	5467	TCGTACTCGAACACAGGAAGGC
436	A	1551_436_A_F_1552_436_A_R	5435	ACCCAGACCCGACTAGGGGAC	5468	GACCGAAGCCAGGATGAG
436	B	1553_436_B_F_1554_436_B_R	5436	TTCCCATCAATTCAATCC	5469	TCAGGCCACGTCAATCATTA
436	C	1555_436_C_F_1556_436_C_R	5437	TTTCTTGGCTCTCCGTGAGT	5470	GAGCGAAAGAAAGTCCACG
436	D	1557_436_D_F_1558_436_D_R	5438	GCCACGTGGACTTTCTTTTC	5471	GGGTGATGTGAAGGAATTGG
436	E	1559_436_E_F_1560_436_E_R	5439	TAGGAGACCCCTGTGACAT	5472	TGAGGCACAGAAATCACTTG
436	F	1561_436_F_F_1562_436_F_R	5440	CTGCACCTGAGGTGACAGAG	5473	ACACCTGGCCACCACTTACT
436	G	1563_436_G_F_1564_436_G_R	5441	TCTCTGAGGTTTTCGTCGCT	5474	GGGATGAGCAGCAGAGACAC
436	H	1565_436_H_F_1566_436_H_R	5442	CAGGTGCTGAGGAAGCCT	5475	TGCCTGAGTGTGCTCTTC

436	I	1567_436_I_F_1568_436_I_R	<u>5443</u>	TGTGCCAGCTCCACTCTAAC	<u>5476</u>	ATGTCAAATTTCCCTGCCTG
436	J	1569_436_J_F_1570_436_J_R	<u>5444</u>	GCCCGTCGAGAAACACTTT	<u>5477</u>	GGTCTTGAGAGGGAAGGT
436	K	1571_436_K_F_1572_436_K_R	<u>5445</u>	CCATTCCGGTAAAGATTCCA	<u>5478</u>	ACACCCAAGAGATGAGAGC
436	L	1573_436_L_F_1574_436_L_R	<u>5446</u>	CTACTTCAGTGCACCTTGGC	<u>5479</u>	ATTCTCTGGGTGATGTGG
436	M	1671_436_M_F_1672_436_M_R	<u>5447</u>	CCATCAGTGTGCTGAGTGCT	<u>5480</u>	ACAGGCTCTTAAATTGCCA
449	A	1971_449_A_F_1972_449_A_R	<u>5448</u>	CCAGATATTCAGCCTCAGC	<u>5481</u>	ATCAGTGCATCTCTGTCCC
449	A	1973_449_A_F_1974_449_A_R	<u>5449</u>	CTGGGTAGGAGCCTGGCTAT	<u>5482</u>	AAATGCTCTGCCTCAGAAA
449	A	1975_449_A_F_1976_449_A_R	<u>5450</u>	GGAAGAGGTGCTAGACGCTG	<u>5483</u>	GCTAGGTGGGATGGGTATT
449	B	1977_449_B_F_1978_449_B_R	<u>5451</u>	AGTGGCCTCAGGGTGAC	<u>5484</u>	TCTCTGCTCCATCTCAGGT
449	B	1979_449_B_F_1980_449_B_R	<u>5452</u>	ATGTGGCAAGCCAGGAC	<u>5485</u>	CCCAAGCATAGGACACAGA
449	C	1981_449_C_F_1982_449_C_R	<u>5453</u>	TCAATCCCAATCTCTTCT	<u>5486</u>	CTCTCCCTCTCTCTTGGC
449	D	1983_449_D_F_1984_449_D_R	<u>5454</u>	CAACGCCATCCTTACACAGA	<u>5487</u>	TGTGAGTGTGTAGTACTTGCTC
449	D	1985_449_D_F_1986_449_D_R	<u>5455</u>	ACTGTGATGACCTGCTCCT	<u>5488</u>	TGTGTGTTGTTGGAGGTC
449	E	1987_449_E_F_1988_449_E_R	<u>5456</u>	CAAACCAATTATGAGCCTGGG	<u>5489</u>	GTCGTTCTGACCTTCAAGCC
449	F	1989_449_F_F_1990_449_F_R	<u>5457</u>	TGTGACTTAACACCTCTCCTC	<u>5490</u>	TGAGTGTGGGAGGAAGATCCC
449	F	1991_449_F_F_1992_449_F_R	<u>5458</u>	GCTCCTTAGCCAAATATGGGA	<u>5491</u>	ATAGATCCCCAGACCACAAC
449	F	1993_449_F_F_1994_449_F_R	<u>5459</u>	ATTCCAAGGCCAAGTCTCTG	<u>5492</u>	TCTGGCCTGGGATTAATCAT
449	F	2011_449_F_F_1992_449_F_R	<u>5460</u>	CAGGTGCTCCTTAGCCAAATA	<u>5493</u>	ATAGATCCCCAGACCACAAC
515	A	1226_515_A_F_1227_515_A_R	<u>5461</u>	GCTCCATCGGACTCAGTAGC	<u>5494</u>	TGGAITTCAGGACTTGAGG
515	A	1228_515_A_F_1229_515_A_R	<u>5495</u>	TGTTGGGCTGGAGTTTATC	<u>5528</u>	TCATGGCAAAACATGAAGAGC
515	A	1230_515_A_F_1231_515_A_R	<u>5496</u>	GCCGTTGCTGATGGACTACT	<u>5529</u>	GCCATTCTGGATCAGCAACT
515	A	1232_515_A_F_1233_515_A_R	<u>5497</u>	CAGCCATCATCTCTTGCCCT	<u>5530</u>	CCACCATGATGAAGGTGATG
515	A	1234_515_A_F_1235_515_A_R	<u>5498</u>	GCATCATCTCTGTTCTGCTCA	<u>5531</u>	TGATAAAGAAGCCAGGTCC
515	A	1236_515_A_F_1237_515_A_R	<u>5499</u>	GGCCATCGTCTTTGTCAICT	<u>5532</u>	GCTCGTGTGCGGTTATTAT
515	A	1238_515_A_F_1239_515_A_R	<u>5500</u>	ACTTCTCAGGCCCATCTTT	<u>5533</u>	GCAACAGCCCAACTGTTTCT
515	A	1240_515_A_F_1241_515_A_R	<u>5501</u>	CATGGAGCCCTCTTATCTG	<u>5534</u>	GCAACCAGTCTCCCACTCAT
570	C	1310_570_C_F_1311_570_C_R	<u>5502</u>	GGTTTCATCTTGAAGACTGT	<u>5535</u>	CCACAGAGGAAGACCACAA
570	C	1312_570_C_F_1313_570_C_R	<u>5503</u>	TAGCGGCAATTGCCATATATT	<u>5536</u>	ACCTTTCAAAACAGCCCAAGA
570	D	1314_570_D_F_1315_570_D_R	<u>5504</u>	TGAGCTGGTTTCTTACCTCA	<u>5537</u>	CAAAGCCAAGAAACAGGGA
570	D	1316_570_D_F_1317_570_D_R	<u>5505</u>	AGGCATTGGAGTCTTTCAGC	<u>5538</u>	AAATGGCCAAAACAAGTGCT
570	E	1318_570_E_F_1319_570_E_R	<u>5506</u>	GAGAGCACAGTTGTTCCACA	<u>5539</u>	ACAAATGCTTTTGTGCGGTG
570	F	1320_570_F_F_1321_570_F_R	<u>5507</u>	CCTGTATTGCGGGGAGTAAA	<u>5540</u>	TCTGAATCCACAACCTGCTGC
570	G	1322_570_G_F_1323_570_G_R	<u>5508</u>	CGAAGTCTCGTAGCCACAATC	<u>5541</u>	GTGCTGGAATCAGACACCT
570	H	1324_570_H_F_1325_570_H_R	<u>5509</u>	CCATGTGTTAAAGTGCCCT	<u>5542</u>	CCCCTCACTGGCTATTTTCA
570	I	1326_570_I_F_1327_570_I_R	<u>5510</u>	GCCTGCATCACTGTGTTTCC	<u>5543</u>	AGAAAGGGAAGCTTGGGGTA
570	I	1516_570_I_F_1517_570_I_R	<u>5511</u>	GGGACGTCCTTGACAGACA	<u>5544</u>	TGGAGCTGTTTTTGTGCATC
570	J	1330_570_J_F_1331_570_J_R	<u>5512</u>	AAAATACCTGTAGCAGCGCA	<u>5545</u>	ATTGGCTCTTGATCGCTGA
570	J	1332_570_J_F_1333_570_J_R	<u>5513</u>	GCTACCCCTCCTGCTTTTCT	<u>5546</u>	ATCAATCCAGGCAACATGC

570	B	1897_570_B_F_1898_570_B_R	<u>5514</u>	TGCTGCTATTCTGACGGG	<u>5547</u>	GCCGTGCAGTTGAGCAGG
581	C	1362_581_C_F_1363_581_C_R	<u>5515</u>	TTCCGTGACTCTGGATCTT	<u>5548</u>	ATGAACCTCAACACCCAAAGG
581	D	1364_581_D_F_1365_581_D_R	<u>5516</u>	GGAAAACTTGCTTGTGAA	<u>5549</u>	TGTTGGAACAGACCTGATTTTC
581	E	1366_581_E_F_1367_581_E_R	<u>5517</u>	TGAGGGAGAGATACAGGTGA	<u>5550</u>	TGTTGCCACACAAACAAATG
581	E	1368_581_E_F_1369_581_E_R	<u>5518</u>	ACAAGAATGTGCCTAAC TGCC	<u>5551</u>	GACTCCGCTTTGGGAAAA
581	F	1370_581_F_F_1371_581_F_R	<u>5519</u>	ACCATGCCCTGCCAAGAA	<u>5552</u>	GCTCATACTGTGCTGCCAAA
581	F	1524_581_F_F_1525_581_F_R	<u>5520</u>	CAGTACTACGACATTTCTGCCAA	<u>5553</u>	GGAATAAACAAAGCCAAACCG
581	G	1374_581_G_F_1375_581_G_R	<u>5521</u>	GATTGTTGGGTTTGCTTGT	<u>5554</u>	TCAGCATCCACAGATGAAG
698	A	1334_698_A_F_1335_698_A_R	<u>5522</u>	GACCAGAATCCCAAGAGCAC	<u>5555</u>	TGCTGTGATTGCCCTAACAA
698	B	1336_698_B_F_1337_698_B_R	<u>5523</u>	TTTGCCCACTGAGATGCTA	<u>5556</u>	AAATCCAGTGGCTTCCTTCC
698	C	1338_698_C_F_1339_698_C_R	<u>5524</u>	ACTGCTTTGCTCCTGGGAA	<u>5557</u>	CACAAAACTGAAACCCTGCC
698	E	1342_698_E_F_1343_698_E_R	<u>5525</u>	TGTTTGGCTTGATCACTGAGA	<u>5558</u>	TGACTGCCAAGCAATTTTCA
698	F	1344_698_F_F_1345_698_F_R	<u>5526</u>	AGGAAGGTGTTTAIGCACGG	<u>5559</u>	GCTCTTACACCGAAAACTGC
698	G	1520_698_G_F_1521_698_G_R	<u>5527</u>	CAGGTGAGTTTAGTTTCTGTCC	<u>5560</u>	CCTCCATCTTGCAGTTCAI
698	G	1522_698_G_F_1523_698_G_R	<u>5561</u>	TCAGGTTGCTGCTGTTGTCA	<u>5594</u>	AAACGGCAICTAACCAITTAATC
698	H	1348_698_H_F_1349_698_H_R	<u>5562</u>	CATCCCCGTAGTTTGATTT	<u>5595</u>	CTCAGTGGCACCCACAGTAG
698	I	1350_698_I_F_1351_698_I_R	<u>5563</u>	TCCTGCTCCTTCTGTGAAGG	<u>5596</u>	TTTCTGGAAGACCCCAAGTTT
698	J	1352_698_J_F_1353_698_J_R	<u>5564</u>	TGTGTCGTAGGCATGAATTG	<u>5597</u>	CCCTCATCTTTTCATCTTGTG
698	K	1354_698_K_F_1355_698_K_R	<u>5565</u>	GGAGCATGTGAACACCTGAA	<u>5598</u>	GAAACCACCAACCAAGGAGAA
698	L	1356_698_L_F_1357_698_L_R	<u>5566</u>	AGTTTTCAGCACATCCGTGT	<u>5599</u>	GCCTTTTAAACCACACGCTATTTG
698	M	1358_698_M_F_1359_698_M_R	<u>5567</u>	TTGACCTACAAGCTGTGCCA	<u>5600</u>	CTCTGGCCAACAAGAAAAAGC
698	M	1360_698_M_F_1361_698_M_R	<u>5568</u>	TCCTTCCACTAAAGGGTGTA	<u>5601</u>	TCCTAATCCCTTCCCAAGT
698	D	1518_698_D_F_1519_698_D_R	<u>5569</u>	TGTGCTTCTTGTGCTGTCTCT	<u>5602</u>	ACCATTTGTTATTCGGGGCT
702	A	630_702_A_F_631_702_A_R	<u>5570</u>	GGCCAGGGACATCAGGTT	<u>5603</u>	GTCTGCAGCTGCCCTGTT
702	A	632_702_A_F_633_702_A_R	<u>5571</u>	CCCCTCACCCTGCTCTCT	<u>5604</u>	CATAAGACGGGACTGTGCCT
702	B	634_702_B_F_635_702_B_R	<u>5572</u>	AGTGAGCTGGGCTAGGCTCT	<u>5605</u>	GGAGACCCCGTTCTCTCAC
702	C	636_702_C_F_637_702_C_R	<u>5573</u>	CTGCTCCTCATCTCACAGG	<u>5606</u>	CCCTGAACCTTCACGAGGT
702	C	638_702_C_F_639_702_C_R	<u>5574</u>	GTGGAAGGGGTAGCCGTC	<u>5607</u>	CCTGTTCTCCGTGACTCACTC
702	D	640_702_D_F_641_702_D_R	<u>5575</u>	GGGGTTTCTGACCCCTCTT	<u>5608</u>	CAGTGGCTGTCCACGAGTT
702	D	642_702_D_F_643_702_D_R	<u>5576</u>	ACCTTGTCTCTGTAAGGGAG	<u>5609</u>	GCCCTTCTTGCCCTTAGTTC
702	E	644_702_E_F_645_702_E_R	<u>5577</u>	CAGAGCCTGTCTGTGAGTG	<u>5610</u>	GGACAGGGATGAGGACAGAC
702	F	646_702_F_F_647_702_F_R	<u>5578</u>	CACACAAGGATGCCTGTCC	<u>5611</u>	GGTCTGCACCCAGAGAGTG
702	G	648_702_G_F_649_702_G_R	<u>5579</u>	TGGGTGCAGACCGTCTCT	<u>5612</u>	CTCCATGAGCGGACAGAGA
702	H	650_702_H_F_651_702_H_R	<u>5580</u>	CTTGGCTGCCCTGTAGTGAT	<u>5613</u>	CATCGACGCTGCCCTTCTC
702	H	652_702_H_F_653_702_H_R	<u>5581</u>	CCTCGTGTGTGTCATCGTAAC	<u>5614</u>	GGCTGACACAGAGAGAAGAA
702	I	654_702_I_F_655_702_I_R	<u>5582</u>	CGAGGGTACCCACTCCCAT	<u>5615</u>	ACCAACCCCAACCCACACT
702	I	656_702_I_F_657_702_I_R	<u>5583</u>	AGCAGGGAGAGGTGATGTTG	<u>5616</u>	CAGAAAGGTGCCCAGTCA
702	I	658_702_I_F_659_702_I_R	<u>5584</u>	CCGAGATGCTCCCTCCAG	<u>5617</u>	CACAGAGGGCAAGGACTGTG

702	I	660_702_I_F_661_702_I_R	5585	TCGTCAGTCAACACAGTCCC	5618	CCAGGCCCTGACCGTATG
702	I	662_702_I_F_663_702_I_R	5586	CACAGTCCTTGCCCTGTG	5619	GCCCCCAGGACAACAT
702	I	664_702_I_F_665_702_I_R	5587	GTGCATGAGCAGACCTCGTA	5620	TGCCCTCCTACTTCTCCGTG
702	I	666_702_I_F_667_702_I_R	5588	CTCCACACACCAGCCAGTC	5621	CAGTCCTGTGCAAGCCCC
722	B	382_722_B_F_510_722_B_R	5589	TTCAAGTCGCTAATTTGTGCC	5622	GGACAGGTAGGCAAGGCTATG
722	C	813_722_C_F_814_722_C_R	5590	GATTGAGTTGCCATGCTGT	5623	ACAGCCAGAGGGACACACA
722	D	386_722_D_F_387_722_D_R	5591	ATGTTGATATTATAGCTCAGATGC	5624	CAAAATACCATACTCCCAACATC
722	E	388_722_E_F_389_722_E_R	5592	TTGAAGTCAGGCTTGAACA	5625	TTCAGAGTCTGCAAGAGAAGAGT
722	F	390_722_F_F_391_722_F_R	5593	ATGCCCTCAGATACGAATG	5626	TTGAAGTGAGACCTTAAAGGAGA
722	G	512_722_G_F_513_722_G_R	5627	ATGGTTGCAAAATGGCTTTGT	5652	ACAGAGAGAGACATGGAGCC
722	H	394_722_H_F_395_722_H_R	5628	CCCTTTAACCTTCCAACCCA	5653	TCTTGAGAATGCAAGAGTCTG
722	I	396_722_I_F_397_722_I_R	5629	CCATTACATGCACATCGTGT	5654	TCTTGAAAGCCAACCTCACC
722	J	1526_722_J_F_1527_722_J_R	5630	GCAAAATGCCAATGTGATTT	5655	CGGGTTACAGCGCTGAGAT
722	AA	739_722_AA_F_740_722_AA_R	5631	TCAGCTTGCTTTTCTTTGACA	5656	GTGGCTGGCAAGCTTTTATT
722	A	1901_722_A_F_1902_722_A_R	5632	GGGCTCCCGCTGGAAG	5657	GGCCTGAACCGCTACCC
748	A	1995_748_A_F_1996_748_A_R	5633	TAGCATCCACCTGTGCTCC	5658	CAGAAGCCAGAAAGGCAAG
748	A	1997_748_A_F_1998_748_A_R	5634	GCTTCATGGTTGCTTAAAA	5659	TGCCTTTCAATCAGTAGAAGAAC
748	A	1999_748_A_F_2000_748_A_R	5635	TAAGAAATGGGTTGAGGGTG	5660	TGGTTGAGAGAGCAAGAGGAA
751	U	1945_751_U_F_1946_751_U_R	5636	GGTGCTACCTCCTCTGATCCT	5661	CACCTGCAGCCTCATGTGA
751	V	1947_751_V_F_1948_751_V_R	5637	TAGCCTGTGGTGAGGGCAGT	5662	TCCTGTGACCTCAAAAGCATCC
751	W	1949_751_W_F_1950_751_W_R	5638	TGCCACTCAGGGTGACTGT	5663	TGCAAGCCTGCTCCTGAT
751	X	1951_751_X_F_1952_751_X_R	5639	CCTAACCTACGTGCAAAAGGCG	5664	GCTCAGGATTTGAGTCCAG
751	Y	1953_751_Y_F_1954_751_Y_R	5640	ATTTCAAATCCCAACCTCC	5665	CTGGAGCCCTCGGTTATG
751	Z	1955_751_Z_F_1956_751_Z_R	5641	TCACTGGGCTTATGGCTCTC	5666	GTCCATGAGCAAAAGGTGAG
848	Y	2001_848_Y_F_2002_848_Y_R	5642	GCCCTCAACTTTGCCCTCTC	5667	TAAACGCAAAATCCACCTC
848	Y	2003_848_Y_F_2002_848_Y_R	5643	TCTCCTCGCCCTCTCTCTG	5668	TAAACGCAAAATCCACCTC
848	Z	2004_848_Z_F_2005_848_Z_R	5644	CATTGTCTTCACTGGCCG	5669	TGGTGTCTGCCGCTGATT
GenR2	A	1453_GenR2_A_F_1454_GenR2_A_R	5645	CCAGCCCCCAAAATTAAAGTG	5670	CCTCTCGCCTAAAACTGTGC
GenR2	B	1455_GenR2_B_F_1456_GenR2_B_R	5646	CATTTCTTGACACACAATGG	5671	TGGTTGAGCCACCATACTCA
GenR2	C	1457_GenR2_C_F_1458_GenR2_C_R	5647	TATTTCAACCAGGAGGTTG	5672	TGTTGCCAAGAATGTGAAA
GenR2	D	1459_GenR2_D_F_1460_GenR2_D_R	5648	TCCTCTAGGAACAGAGCCA	5673	ATGCACTCAGCGACCTTCTC
GenR2	F	1575_GenR2_F_F_1576_GenR2_F_R	5649	GTCCTTCCCATCCCTCAACA	5674	GGGAGGCATAATGAACGAGA
GenR2	F	1577_GenR2_F_F_1578_GenR2_F_R	5650	TAGCGCCCTATCCCTTTCTT	5675	TCCATCCCAAGCTTCACTCT
GenR2	E	1790_GenR2_E_F_1791_GenR2_E_R	5651	CTCTGACCTTGCACTACCCC	5676	CCACCGTGCTCTTCAAAATTCA

Please replace Table 9 on pages 178-181 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 9: SEQUENCING PRIMERS

			SEQ ID NO.		SEQ ID NO.
Gene	Exon	Forward Primer	Forward Sequence	Reverse Primer	Reverse Sequence
454	B	MDSseq_118_454_B_F	CCAGATACTGGCAAGGAG	MDSseq_118_454_B_R	GCACCAGGACATGAGGCTAT
454	E	MDSseq_119_454_E_F	AGCCAGCAGGAATCCACAGTC	MDSseq_119_454_E_R	GGTACCCCTGGAAGATCTGGG
454	E	MDSseq_473_454_E_F	TCCTGTACTCTCCTGCGGT	MDSseq_473_454_E_R	CCAAGTCACGCAAGAATGA
454	F	MDSseq_120_454_F_F	ACAGCAAGGAGGAAGTCCG	MDSseq_120_454_F_R	TGAAAAAGGTTCTCCAGC
454	G	MDSseq_121_454_G_F	TTCTCCAGAGCAAGTGACC	MDSseq_121_454_G_R	CCACAGGAAAGGAATACACCA
454	H	MDSseq_122_454_H_F	AGTGCCCTGAATTCAGTCT	MDSseq_122_454_H_R	CATTGATCTTGTGCCTTGG
454	H	MDSseq_291_454_H_F	AGTGCCCTGAATTCAGTCT	MDSseq_291_454_H_R	CATTGATCTTGTGCCTTGG
454	K	MDSseq_123_454_K_F	CCCAGAACCCAGCACATTTC	MDSseq_123_454_K_R	TAGAAATTGCTTCCAGGCCC
454	L	MDSseq_124_454_L_F	GTCCTCCCTTAATGTGTGGG	MDSseq_124_454_L_R	GGGCCCTAATTTTCGTGCAT
454	M	MDSseq_125_454_M_F	CCAGCAGCTTGAACGCATCTA	MDSseq_125_454_M_R	CTTCCCTCTATCTTGCCCT
454	N	MDSseq_126_454_N_F	AGCATGGGGTTCCCATTTT	MDSseq_126_454_N_R	ATTGGAAGGGGGCATAAAG
454	O	MDSseq_127_454_O_F	CGATTCTTGACACAACCCAGA	MDSseq_127_454_O_R	GGACAGTTTGCTGTGCTC
454	O	MDSseq_128_454_O_F	GAACACATGCATGTGCTCTGA	MDSseq_128_454_O_R	ACAGACAGGATTCGCCCTTG
454	AA	MDSseq_460_454_AA_F	CTCAACTCCACTTTCCTCGG	MDSseq_460_454_AA_R	CAAGAAGCGGCCAAGTCTAC
454	AA	MDSseq_470_454_AA_F	TGCATCTTTGAGTGAAGTGTG	MDSseq_470_454_AA_R	ACTCTGCTCTGCAGTTGCTG
454	AA	MDSseq_471_454_AA_F	TCTGTGACATTTGCAAGGC	MDSseq_471_454_AA_R	TCAGAAATGTGCACCTGAAGC
757	A	MDSseq_407_757_A_F	CTCGCTTCCCGGTATTGTT	MDSseq_407_757_A_R	GCCTCCATGCACAGGTAGTT
757	A	MDSseq_408_757_A_F	TTCTTCTGTGCTGCTGTGA	MDSseq_408_757_A_R	CTCTCAGTCCCTCCTCGAT
757	A	MDSseq_409_757_A_F	CGTGAGCGTGTACTGAGC	MDSseq_409_757_A_R	CTCCAGCTTGTCGCTGTTCT
757	A	MDSseq_410_757_A_F	AGCCAACAGCAGCTACTTCC	MDSseq_410_757_A_R	GACTGGGCGAGGATCTCATA
757	A	MDSseq_411_757_A_F	TCTTTATGCTGCTGTTGGTG	MDSseq_411_757_A_R	GGGTCTGTCTTCTCTCTGC
757	A	MDSseq_412_757_A_F	AGGGAAGCTCCTCCAGTGA	MDSseq_412_757_A_R	TCTGCCAACCTAGTGTCTCC
757	A	MDSseq_413_757_A_F	TGAAGTCAACGATGTGCAA	MDSseq_413_757_A_R	TTCCAACCTTCACACATTGCC
757	A	MDSseq_418_757_A_F	CTCGCTTCCCGGTATTGTT	MDSseq_418_757_A_R	GCCTCCATGCACAGGTAGTT
757	A	MDSseq_419_757_A_F	AGGGAAGCTCCTCCAGTGA	MDSseq_419_757_A_R	TCTGCCAACCTAGTGTCTCC
757	A	MDSseq_421_757_A_F	CAAACCTTGCTGCTCTCCG	MDSseq_421_757_A_R	AGTTGGGCTGTTCTTGTG
757	A	MDSseq_422_757_A_F	CAAGGAAGAGCGCCGAAGTTTG	MDSseq_422_757_A_R	TACAGCGAGCACAGGAAGAA
757	A	MDSseq_423_757_A_F	GAGGACACGTCACACGCC	MDSseq_423_757_A_R	CTCGTCCGAGCCGTTGTT
757	A	MDSseq_424_757_A_F	CAAGAAGAGGCGCGAAGTTTG	MDSseq_424_757_A_R	TACAGCGAGCACAGGAAGAA
757	A	MDSseq_425_757_A_F	GAGGACACGTCACACGCC	MDSseq_425_757_A_R	CTCGTCCGAGCCGTTGTT
561	B	MDSseq_169_561_B_F	ACTGCTCTCCCGTGAAAGTGTG	MDSseq_169_561_B_R	CCATCAGCATCTGTGTGACC

561	C	MDSseq_170_561_C_F	TTAGCCCAAGGAAAGGAGCA	<u>5734</u>	MDSseq_170_561_C_R	CCTCGATGGGATTGCTTT	<u>5766</u>
561	E	MDSseq_171_561_E_F	ATCTGTGTGTGAGCTGGC	<u>5735</u>	MDSseq_171_561_E_R	GGGTGCTGAAGACAGAGC	<u>5767</u>
561	H	MDSseq_172_561_H_F	AAATGGTTGACGTCACCTGGC	<u>5736</u>	MDSseq_172_561_H_R	CTGTGGCTGTGGCAGGAT	<u>5768</u>
561	J	MDSseq_173_561_J_F	TGTTGGAGCTGAGAGACCTG	<u>5737</u>	MDSseq_173_561_J_R	CCTCTAAACTCCTTTACCAGACC	<u>5769</u>
561	H	MDSseq_174_561_H_F	CTCTGGGCAGAGGACTGGT	<u>5738</u>	MDSseq_174_561_H_R	TGACAGAGTCCACCAGCAAA	<u>5770</u>
561	M	MDSseq_177_561_M_F	ACCCTGCCCTGATGAGAGAA	<u>5739</u>	MDSseq_177_561_M_R	TGTTTGCAAGCAAGACGGTA	<u>5771</u>
561	P	MDSseq_183_561_P_F	AGGCAGATTCTCAGCTCCT	<u>5740</u>	MDSseq_183_561_P_R	CAGAGGGCAAAATAACCTCCA	<u>5772</u>
561	G	MDSseq_390_561_G_F	GCATTTCCAGAGAAGATGGTG	<u>5741</u>	MDSseq_390_561_G_R	TAATCCAGAGCAGAGCAGGG	<u>5773</u>
561	H	MDSseq_392_561_H_F	CTCTGGGCAGAGGACTGGT	<u>5742</u>	MDSseq_392_561_H_R	TGACAGAGTCCACCAGCAAA	<u>5774</u>
561	X	MDSseq_401_561_X_F	GAACTGCCCTGTCCATCTGT	<u>5743</u>	MDSseq_401_561_X_R	AAATCTCAGGCTGGAGGAC	<u>5775</u>
561	Y	MDSseq_402_561_Y_F	ACAACTCCAATTGGCGAGAA	<u>5744</u>	MDSseq_402_561_Y_R	CCAAGCAGAGATAACCAAGCA	<u>5776</u>
561	X	MDSseq_415_561_X_F	GAACTGCCCTGTCCATCTGT	<u>5745</u>	MDSseq_415_561_X_R	AAATCTCAGGCTGGAGGAC	<u>5777</u>
561	X	MDSseq_417_561_X_F	GAACTGCCCTGTCCATCTGT	<u>5746</u>	MDSseq_417_561_X_R	AAATCTCAGGCTGGAGGAC	<u>5778</u>
214	B	MDSseq_15_214_B_F	GACAGTCTGCTCCACATCCA	<u>5747</u>	MDSseq_15_214_B_R	TGGAGATGAAGTCTTGCTCT	<u>5779</u>
214	C	MDSseq_110_214_C_F	ATATGTTTGCTGGCTTTGGG	<u>5748</u>	MDSseq_110_214_C_R	CCAGGCTGTGTCTCTCTA	<u>5780</u>
214	E	MDSseq_343_214_E_F	TGCTTCCTGTTTGTACTGC	<u>5749</u>	MDSseq_343_214_E_R	TGAGGACACGATGAACCTGA	<u>5781</u>
214	E	MDSseq_383_214_E_F	ATGGACCTGGGTGAGGACTT	<u>5750</u>	MDSseq_383_214_E_R	GCAGTGACAAACAGGAAGCA	<u>5782</u>
214	AA	MDSseq_399_214_AA_F	CGAATAAAGGCGTCGAGAAAG	<u>5751</u>	MDSseq_399_214_AA_R	CCTTCCTGAGAGGACCGTG	<u>5783</u>
224	BB	MDSseq_403_224_BB_F	AATTGACTTTCCCGCCTTCT	<u>5752</u>	MDSseq_403_224_BB_R	GCCCAAGCCATCCTTCTACTT	<u>5784</u>
422	E	MDSseq_431_422_E_F	AAGCATCTTGGCGAAGTCAT	<u>5753</u>	MDSseq_431_422_E_R	AAAGGAGACACTGCCAGAA	<u>5785</u>
422	F	MDSseq_434_422_F_F	TGGGCATCCTGATGACTTG	<u>5754</u>	MDSseq_434_422_F_R	GTGTGCATGCCATATGCTC	<u>5786</u>
422	C	MDSseq_323_436_C_F	TGTGAAAAAGTGTGCTCTGAA	<u>5755</u>	MDSseq_323_436_C_R	AGTTTGGGTGACAGAGCG	<u>5787</u>
422	D	MDSseq_324_436_D_F	TGTGAAAAAGTGTGCTCTGAA	<u>5756</u>	MDSseq_324_436_D_R	AGTTTGGGTGACAGAGCG	<u>5788</u>
422	E	MDSseq_325_436_E_F	TCTTTAGCTTGGCATCACCC	<u>5757</u>	MDSseq_325_436_E_R	ACGCAGAGTTGAAGGTGCTT	<u>5789</u>
422	G	MDSseq_326_436_G_F	CTGCACCTCGAGGTGACAGAG	<u>5758</u>	MDSseq_326_436_G_R	AGCCAGAGATACGTTGTGC	<u>5790</u>
422	K	MDSseq_327_436_K_F	GCTAGGCATGTGAGTGTT	<u>5759</u>	MDSseq_327_436_K_R	CGCAAGGTGCACCTGAAGTAG	<u>5791</u>
422	B	MDSseq_340_436_B_F	CCATCAGTGTGCTGAGTGCT	<u>5760</u>	MDSseq_340_436_B_R	ACCCAAATGTGGAAGGTG	<u>5792</u>
422	L	MDSseq_374_436_L_F	GCACAGGCCCTCTCATCTCTT	<u>5793</u>	MDSseq_374_436_L_R	AGAGTTGACCCAGCCAAAGAA	<u>5825</u>
422	A	MDSseq_375_436_A_F	CAAGATTCTCTCACCCTCGG	<u>5794</u>	MDSseq_375_436_A_R	AACAGCAGCAAGCAGCCT	<u>5826</u>
422	C	MDSseq_393_436_C_F	TCACTGTTTTCATTGGGTTA	<u>5795</u>	MDSseq_393_436_C_R	GTAGGGCAAGAGCTGGGATG	<u>5827</u>
422	D	MDSseq_394_436_D_F	TCACTGTTTTCATTGGGTTA	<u>5796</u>	MDSseq_394_436_D_R	GTAGGGCAAGAGCTGGGATG	<u>5828</u>
422	G	MDSseq_395_436_G_F	GGCTGCAGAAACCTCACCTCT	<u>5797</u>	T MDSseq_395_436_G_R	TGAGTGCTGCTCTTCAGTGG	<u>5829</u>
422	A	MDSseq_396_436_A_F	GCTGGGATGACAGGTGTGAG	<u>5798</u>	MDSseq_396_436_A_R	TCCCAAGTGTCTCGGATTAC	<u>5830</u>
422	A	MDSseq_404_436_A_F	AGGAGCCCTTTCGCTCTCAA	<u>5799</u>	MDSseq_404_436_A_R	ATGTTGCCCAAAATTGGTTTC	<u>5831</u>
422	D	MDSseq_414_436_D_F	TCACTGTTTTCATTGGGTTA	<u>5800</u>	MDSseq_414_436_D_R	GTAAGGCAAGAGCTGGGATG	<u>5832</u>
422	D	MDSseq_416_436_D_F	TCACTGTTTTCATTGGGTTA	<u>5801</u>	MDSseq_416_436_D_R	GTAAGGCAAGAGCTGGGATG	<u>5833</u>
436	C	MDSseq_323_436_C_F	TGTGAAAAAGTGTGCTCTGAA	<u>5802</u>	MDSseq_323_436_C_R	AGTTTGGGTGACAGAGCG	<u>5834</u>

436	D	MDSseq_324_436_D_F	TGTGAAAAGTGTGCTCTGAA	<u>5803</u>	MDSseq_324_436_D_R	AGTTGGGTGACAGAGCG	<u>5835</u>
436	E	MDSseq_325_436_E_F	TCTTAGCTTGGCATCACCC	<u>5804</u>	MDSseq_325_436_E_R	ACGCAGAGTTGAAGGTGCTT	<u>5836</u>
436	K	MDSseq_327_436_K_F	GCTAGGCATGTGAGTGGTT	<u>5805</u>	MDSseq_327_436_K_R	CGCAAGGTGCACCTGAAGTAG	<u>5837</u>
436	B	MDSseq_340_436_B_F	CCATCAGTGTGCTGAGTGCT	<u>5806</u>	MDSseq_340_436_B_R	ACCCAAAATGTGAAAGCTG	<u>5838</u>
436	L	MDSseq_374_436_L_F	GCACAGGCCCTCTCATCTCTT	<u>5807</u>	MDSseq_374_436_L_R	AGAGTTGACCCAGCCAAAGAA	<u>5839</u>
436	C	MDSseq_393_436_C_F	TCACTGTTTTCCATTGGGTTA	<u>5808</u>	MDSseq_393_436_C_R	GTAGGGCAAGAGCTGGGATG	<u>5840</u>
436	D	MDSseq_394_436_D_F	TCACTGTTTTCCATTGGGTTA	<u>5809</u>	MDSseq_394_436_D_R	GTAGGGCAAGAGCTGGGATG	<u>5841</u>
436	G	MDSseq_395_436_G_F	GGCTGCAGAAAACCTCACTCT	<u>5810</u>	T MDSseq_395_436_G_R	TGAGTGTGCTGCTTTCAGTGG	<u>5842</u>
436	A	MDSseq_404_436_A_F	AGGAGCCCTTCGTCTCAA	<u>5811</u>	MDSseq_404_436_A_R	ATGTTGCCCAAAATTGGTTTC	<u>5843</u>
436	D	MDSseq_414_436_D_F	TCACTGTTTTCCATTGGGTTA	<u>5812</u>	MDSseq_414_436_D_R	GTAGGGCAAGAGCTGGGATG	<u>5844</u>
436	D	MDSseq_416_436_D_F	TCACTGTTTTCCATTGGGTTA	<u>5813</u>	MDSseq_416_436_D_R	GTAGGGCAAGAGCTGGGATG	<u>5845</u>
449	D	MDSseq_462_449_D_F	GTCACACAGCCAGTAGGCAG	<u>5814</u>	MDSseq_462_449_D_R	CAGAGAGCAAGAAAGGCCAAG	<u>5846</u>
449	F	MDSseq_463_449_F_F	AAGAGAAAATCCGGAGGACC	<u>5815</u>	MDSseq_463_449_F_R	ACGGGCTCTCCCTGTGATA	<u>5847</u>
449	A	MDSseq_472_449_A_F	CCAACCTCAGTTTCCCAACG	<u>5816</u>	MDSseq_472_449_A_R	CAGGAGCGTGAGCTCTGATA	<u>5848</u>
449	F	MDSseq_474_449_F_F	CACATATCTGCCCTGCTCCT	<u>5817</u>	MDSseq_474_449_F_R	CACCATCAGGATTCTTCACG	<u>5849</u>
515	A	MDSseq_235_515_A_F	CAGCCATCATCTCTTGCCCT	<u>5818</u>	MDSseq_235_515_A_R	ATTACTCGATGCAACAGCCC	<u>5850</u>
515	A	MDSseq_236_515_A_F	TGGACCTGGCGTTCTTATC	<u>5819</u>	MDSseq_236_515_A_R	CAGGAGCAACACAATTCCCT	<u>5851</u>
515	A	MDSseq_237_515_A_F	CGTAGTTTCTCTGTACCAATTCA	<u>5820</u>	MDSseq_237_515_A_R	TTGGAGATCTTGTTCAGGGC	<u>5852</u>
515	A	MDSseq_239_515_A_F	GGCCATCGTCTTTGTATCT	<u>5821</u>	MDSseq_239_515_A_R	CGGTCAGAGATGAAGCAAGT	<u>5853</u>
515	A	MDSseq_263_515_A_F	CTGCTGTGTGTTCCGAGATG	<u>5822</u>	MDSseq_263_515_A_R	GTGTGCAGAGGCCAGAAGAT	<u>5854</u>
515	A	MDSseq_265_515_A_F	GGCCATCGTCTTTGTATCT	<u>5823</u>	MDSseq_265_515_A_R	GGCTCAGAGATGAAGCAAGT	<u>5855</u>
570	C	MDSseq_266_570_C_F	TTGATTGTGTGCGCTTCTT	<u>5824</u>	MDSseq_266_570_C_R	GCATGAGCTCTGGAATCAGG	<u>5856</u>
570	F	MDSseq_268_570_F_F	CACCTGATTATTTTCCCTCA	<u>5857</u>	MDSseq_268_570_F_R	AACCTCCCTTTAACTCAGTC	<u>5889</u>
570	I	MDSseq_270_570_I_F	CTGAGTGAGCGGAGGTGTTT	<u>5858</u>	MDSseq_270_570_I_R	TTGGCAATTTCTTTCATCAG	<u>5890</u>
570	J	MDSseq_271_570_J_F	CAGACAGCCCACTCCAG	<u>5859</u>	MDSseq_271_570_J_R	CCAAGACTTTGCAATCTCCA	<u>5891</u>
570	I	MDSseq_294_570_I_F	GCTGGCACGTGTTCTATCA	<u>5860</u>	MDSseq_294_570_I_R	CCACGTAGGAATGGAGCTGT	<u>5892</u>
581	E	MDSseq_277_581_E_F	GGGAGATTGATAGGGTACGC	<u>5861</u>	MDSseq_277_581_E_R	TAGCCAGGCGTGTGTA	<u>5893</u>
581	F	MDSseq_345_581_F_F	CCTTCTGAGTAGCTGGGCTC	<u>5862</u>	MDSseq_345_581_F_R	TAGACTTCTGACGCTGGGCT	<u>5894</u>
698	B	MDSseq_274_698_B_F	TGTCTTGACCATCACAGTT	<u>5863</u>	MDSseq_274_698_B_R	CGGCTAAGTCTTTCATCACG	<u>5895</u>
698	E	MDSseq_275_698_E_F	GTAAGCATTTGTGGCAGC	<u>5864</u>	MDSseq_275_698_E_R	TGCCAAGGGCTGTTCTAAT	<u>5896</u>
698	H	MDSseq_280_698_H_F	TGTGTACAGATTGCCCTACCC	<u>5865</u>	MDSseq_280_698_H_R	TGACGAATACAGGATGAAGTC	<u>5897</u>
698	I	MDSseq_287_698_I_F	GACAGCGCCTCTGGGATTA	<u>5866</u>	MDSseq_287_698_I_R	TGAACACAGGCCACAGAAAGTTT	<u>5898</u>
702	C	MDSseq_111_702_C_F	GTGATGAGGACAAGCTCGG	<u>5867</u>	MDSseq_111_702_C_R	ACGTTCCACGGGACTCA	<u>5899</u>
702	D	MDSseq_112_702_D_F	CAACCCTGCCCTGTCTAAT	<u>5868</u>	MDSseq_112_702_D_R	CGCTCCATGAATGTACAAA	<u>5900</u>
702	A	MDSseq_113_702_A_F	TTCCCAACCACTCTCTGTC	<u>5869</u>	MDSseq_113_702_A_R	AAGGGTGGAGGCCCTGAC	<u>5901</u>
702	B	MDSseq_114_702_B_F	CCCTCTGATCAGGACAGATC	<u>5870</u>	MDSseq_114_702_B_R	GGATATCTACAGCAGGCCCA	<u>5902</u>
702	F	MDSseq_115_702_F_F	ACGCTTCTTGTAGGACCGAA	<u>5871</u>	MDSseq_115_702_F_R	AAGACGATCTTGTGTCGCT	<u>5903</u>

702	I	MDSseq_116_702_I_F	AGCAGGGAGAGGTCATGTTG	<u>5872</u>	MDSseq_116_702_I_R	GGTGTGTGAGACTCACAGG	<u>5904</u>
702	I	MDSseq_117_702_I_F	CACTAGGGGACAGCTCCGT	<u>5873</u>	MDSseq_117_702_I_R	CTGCCATCTAGCAGAGCC	<u>5905</u>
702	B	MDSseq_178_702_B_F	AGGCACAGTCCCGTCTTATG	<u>5874</u>	MDSseq_178_702_B_R	GAGAGCTCCTGCTGTCT	<u>5906</u>
702	I	MDSseq_179_702_I_F	TCGTACGTCAACACAGTCCC	<u>5875</u>	MDSseq_179_702_I_R	CCCACTGCAGTCTTGTGC	<u>5907</u>
702	C	MDSseq_191_702_C_F	AGATCGGCCCTAGTGGAAAT	<u>5876</u>	MDSseq_191_702_C_R	GCTCTCATTTCCCTCCCTC	<u>5908</u>
702	I	MDSseq_196_702_I_F	CAGTCTTGTGCAAGCCCC	<u>5877</u>	MDSseq_196_702_I_R	CACAGTCCTTGCCCTCTGTG	<u>5909</u>
702	I	MDSseq_269_702_I_F	AGCAGGGAGAGGTCAITGTTG	<u>5878</u>	MDSseq_269_702_I_R	GGTGTGTGAGAGACTCACAGG	<u>5910</u>
722	F	MDSseq_63_722_F_F	TAAGTAGGGTTGTGACCCGGC	<u>5879</u>	MDSseq_63_722_F_R	CACTCTCCCAATCTCCCTGA	<u>5911</u>
722	C	MDSseq_132_722_C_F	ACCTGATAGGTTTCCCGGT	<u>5880</u>	MDSseq_132_722_C_R	ATACAGATGCCCTGGCTCG	<u>5912</u>
722	AA	MDSseq_135_722_AA_F	GACACGATCCTGGCTCTCTG	<u>5881</u>	MDSseq_135_722_AA_R	GCCTGGGTGACACAGCTA	<u>5913</u>
722	B	MDSseq_141_722_B_F	TTCAGCCAGGATCTGTTGTG	<u>5882</u>	MDSseq_141_722_B_R	GGGCTGGGAGTTACCTTAT	<u>5914</u>
722	B	MDSseq_146_722_B_F	TGCAACACACCAGCAGTTTAC	<u>5883</u>	MDSseq_146_722_B_R	ACCTCTACGGCAGGCTGAAT	<u>5915</u>
722	G	MDSseq_150_722_G_F	CAGTGTGCCGAGACATTGTT	<u>5884</u>	MDSseq_150_722_G_R	TGAGTCTCCACAAACATAGC	<u>5916</u>
722	A	MDSseq_441_722_A_F	TATTACCCCAAAGCTGCACCC	<u>5885</u>	MDSseq_441_722_A_R	TCAAGACTCCCTGAGACCC	<u>5917</u>
751	U	MDSseq_455_751_U_F	AGACACTCTCCAGCTCTCGC	<u>5886</u>	MDSseq_455_751_U_R	GCAGGACCCTGGACTACAGA	<u>5918</u>
751	W	MDSseq_456_751_W_F	CTCCCAGGTAAATGCCCTCAA	<u>5887</u>	MDSseq_455_751_W_R	TACTGTCTCTCATTCCACAGC	<u>5919</u>
GenR2	F	MDSseq_420_GenR2_F_F	CCCAGGAGACAGAGGTTTCA	<u>5888</u>	MDSseq_420_GenR2_F_R	CCCAGACTGGCTTTGAACCTC	<u>5920</u>

Please replace Table 10 on pages 183-187 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 10: SNPs

Gene	Exon	PMP Site	Location	Sequence	SEQ ID NO	PMP	AA change
214	B	1	3' UTR	CCTGTGCACTCTTGGGCAATAGCCCTAGGAGTGAAGTGTG	5921	C>T	
214	C	-1	Intron	GGGCTCTGGCCACCTCAACCCAGGCGTTGTTCCGACAGA	5922	C>T	
214	E	+1	Intron	AAGGACACATTCTATCAGCTGTAGTCACCACGTTCAATTAC	5923	T>C	
214	E	+2	Intron	CCCTGTGACCCCTCAACTCCCGGTCCCTCCAGCCCTGACAG	5924	G>C	
214	E	+3	Intron	CTCAACTCCCGGTCCCTC**CAGCCCTGACAGCCACTGTT	5925	**>TC	
214	E	-1	Intron	AGGCCGCTTCAACCCCTTCTCTCGGGCAGGGGCAATGGCCAA	5926	C>T	
214	E	1	Exon	CACCTGCATTCCCTCTCTCTGTGAGTGTCTGGGGCCCGTT	5927	G>T	Val > Leu
214	E	2	3' UTR	GGGCTCTGCCACCTCAACCCAGGCGTTGTTCCGACAGA	5928	C>T	
214	E	3	3' UTR	TCAGGAGCCTGTGCTTGACCCCAATCCGCCCCCAACTC	5929	C>T	Pro > Ser
422	E	1	Exon	CAGACACATGACAACTGCTATGACCAGGCCAAGAAGCTGA	5930	T>C	
422	E	2	Exon	ACCCACACCTATTCTACTGCTGTGCTGTGGCTCGGCAATCAC	5931	G>A	
436	A	+1	Intron	GGCCGCGCGGGGGCGCGCGGGGTGCTGCCCTCGGCTCCGC	5932	G>T	
436	A	+2	Intron	CTGCTTGCTGTCTTTAAAGCCACAGCCCTGGGCCAGGGCC	5933	G>A	
436	A	-1	Intron	CCCTCCGGGGCATCATCCCGGATGACGGCGCCGCCAGCAGG	5934	G>T	
436	A	-2	Intron	GCCCTCCCCCGGGGCCCGG*****CCCCGACCCGCCCGT	5935	*****>CCCCGGG G	
436	A	-3	Intron	TCCTCAAGGGMGAGGCCCACTCCCCCCCCCGGAGTTCCAT	5936	CC>**	
436	A	1	Exon	CGGGCGGGCGGCCCATGGCGGCTGCTGCCCGCGCTGGCG	5937	G>T	Gly > Cys
436	A	2	Exon	TGAACCGCGCGGTGCAACTGCTCATCTGGCCTACGTCATC	5938	C>T	Leu > Phe
436	C	+1	Intron	ATTCCAGATGCGACCACTGTGTAAATCAGATGCCAGCTG	5939	G>A	
436	C	+2	Intron	AACGGTACGAGCTTGTGGCCCTCTGGGAGGGCAGCCCTG	5940	T>C	
436	C	+3	Intron	TGTGGCCTCTGGGGAGGGCAAGCCCTGAGCAGATGCCCCC	5941	A>G	
436	C	-1	Intron	CTCTCCGTGAGTCTCTGTAGCGGTGGCTGCCCGTGTCT	5942	C>T	
436	D	-1	Intron	GTCACCTGTGTGTGGGCGCGGCCACAGTGACTTTCTTTT	5943	G>A	
436	D	1	Exon	ATTCAGATGCGACCACTGTGTAAATCAGATGCCAGCTG	5944	G>A	
436	E	1	Exon	TGCGTAGCTTTCAACGGGTCGCTCAAGACGTGTAGGTTGGC	5945	C>T	
436	G	1	Exon	TAGTGAGAAACGACGACACAGTTTCCAGGACATGGCCGTG	5946	A>G	Ser > Gly
436	K	+1	Intron	GGGAGGCCCTTCTGCAGAGGCTGGCACCAGTGTGGCGTGT	5947	C>G	
436	K	+2	Intron	RCGACATCTCARGTTGTTGATGATATGATGCTCTGAGAA	5948	T>A	
436	K	-1	Intron	GCTCACTCTACCCCTATGCTAAACTCAGGGCAGCCGTGTGT	5949	A>G	
436	K	-2	Intron	GATTCCAGGCTTCTCAGGAAGGGGCACGCAAGAATAAGAT	5950	G>C	

436	L	-1	Intron	CCAGGAGCGCACCTCCCTCCGCGCTGCCACAAAGGGTCCCA	5951	C>T	
436	L	-2	Intron	GGTGAAGTCCAGGAGCGCACCTCCCTCCGCGCTGCCACAA	5952	C>A	
436	L	-3	Intron	TGGCGTGGTGTCCCGTTAA CC GGGGCAGTCTGCCACTCT	5953	C>T	
436	L	1	3' UTR	AGCAGCTCCTGTGTGTGTGTGTGAGGATCTGTTGCCACT	5954	T>C	
454	B	-1	Intron	AAGTGCCCTGCATCCTCCAA G CGCCTGCATCCCAACCCGCTGT	5955	C>T	
454	B	1	Exon	AGAGGTGAAGAGGAGATCGTGGAGAAATGAGTGAAGAAGT	5956	T>C	Val > Ala
454	E	-1	Intron	CTCCTGGAGAACGTCCTCTCCGCGAGTCTTTCACATCTGTG	5957	C>T	
454	E	-2	Intron	CAAAGCCTAGTCTCTCGCCCGGGTTGAGTTAATGATGTCC	5958	G>A	
454	E	1	Exon	CCCCTATAGGAATTCAGACC G GAAAGGTGTGTAGTATGAA	5959	G>A	Gly > Arg
454	E	2	Exon	AGACCGGAAGGTGTGTAGTGCATGAAGGGAACCAAGAACCC	5960	C>T	His > Tyr
454	E	3	Exon	TGTGAAGTCTCTGCCCTGGTGGCCCATCGAGGCAGTGAAGA	5961	C>T	
454	F	+1	Intron	TCTACTGCTGAGTAATAATTAATCCCAACCTCAGAAGCCT	5962	T>C	
454	F	-1	Intron	CATGGGCTCCCTCGGTCCCA A CCGTCACATAATGGCAATTT	5963	A>C	
454	F	-2	Intron	GGCCCATGGGCTCCCTCGGTCCCAACCGTCACTAATGGCCA	5964	C>T	
454	F	-3	Intron	TGTAATCCATTTCTCTTCATGCA T CCCAAGACCAAGCCAAAG	5965	C>T	
454	G	-1	Intron	CACCTCCTGGAAAGAGACAGATCTGTGTTTCAATCGAGATGT	5966	A>T	
454	H	-1	Intron	GTTCTTCAATCAGCATTTTTCCTCTA A AAACCTTAAGCAAT	5967	C>T	
454	H	-2	Intron	TTTAGGACAAATGAGTTTAACGGGTGATGTGCCAGACGGGG	5968	G>A	
454	H	1	Exon	CCGTTGGTTCATCAGTCCGCTGCCCAATACAGTTTCCGTC	5969	G>A	Arg > His
454	H	2	Exon	CCGTCCCAATACAGTTTCCGCTGCCCTGACGACAAAGACCA	5970	G>A	Arg > His
454	K	1	Exon	GGA A AACAATGTTGAGAAAGGAGACTGTGATAAAGTCTTCG	5971	G>A	Arg > Gln
454	L	-1	Intron	ATTTCACCTGAGTAAACTCTCCACTCTGTTTTAGGGAGG	5972	C>T	
454	M	2	Exon	CATCGACTTCCTCATCGACA CT TA C TACTCCAGTA C TGCTGC	5973	C>G	Thr > Ser
454	M	+1	Intron	GTTACACAGGACACCAAGACACGGAGAGATTCCATGAATCA	5974	C>T	
454	M	+2	Intron	GTA G TGATACGTGCGCTGGGCTTACCCCGATCAACCAACT	5975	C>T	
454	M	1	Exon	GTCGTGCAATTCCTCCCAAGGCCA CT GTGTTCATCGACTTCCTC	5976	A>G	Thr > Ala
454	O	+1	Intron	CTCAGCTCTGTAATCCCAAGCGCTTTGGAGGCCGAGGCAGG	5977	G>A	
454	O	-1	Intron	ATAAATCATGTAATAATTAATGTA CT TAATAAGTTAATAA	5978	T>C	
454	O	1	Exon	TGGACAACCAAGAGGAGATACAGCTGCTTAGAAAGGAGCGCA	5979	A>G	Gln > Arg
454	O	2	Exon	CCTAGATCCAGGGGATAGCCCGTCTGTGTCAGTGTGAAG	5980	C>T	
454	O	3	Exon	GAGCCACAGGTGCTGAGGAGGAGCTGTGCTGCCGAAAAAGC	5981	A>C	Glu > Ala
454	O	4	Exon	CTCTACCAAGAGCCCTTGCTGGCGCTGGATGTGAATTCAC	5982	G>T	
454	O	5	Exon	GGACATGGCTGACTTTGCAATCCTGCCACAGCTGCTGCCGCT	5983	T>A	Ile > Asn
454	O	6	Exon	AGGATCCGGAAAGAGTTTCCAAAGAGTGAAGGGCAGTACAG	5984	A>G	
515	A	1	Exon	CAGCGTGGTGTGCGGATCCGCATCTTCTGGCTCTGCACCA	5985	G>A	Arg > His
515	A	2	Exon	CGCTGCCTCCAGAGGAAGATGACAGGTGAGCCAGATAATAA	5986	G>A	Met > Ile
515	A	3	Exon	GGCGCTCAGAGGCGTTAATGGCCAACCTCCGTTGAGCCATG	5987	G>C	MET > Ile

515	A	4	Exon	GTCACTGGACTCGGCCCTAAGGTTTTCCTGGAACCTCCAGATT	5988	G>A	Val > Ile
515	A	5	Exon	ACTCCAGATTACAGAAATCTGATTTAGGAAACTGTGGCA	5989	C>G	Ile > MET
515	A	6	3' UTR	CTTCAGATTACAGAAATCTGATTTAGGAAACTGTGGCAG	5990	T>C	
515	A	7	Exon	CTGGTTGCAAGGTGTGACCACAGGAATCCTGGAGAACAGA	5991	A>G	
561	B	+1	Intron	TGTGGTGGGAGAGAAATGGCCGTTGGCTGCCCTGGAGGGTG	5992	C>T	
561	B	+2	Intron	CGAGGGTGTGCACAGAGTGAATCGGTTTGGTGACACCTGGC	5993	A>G	
561	B	1	Exon	AAGTCCGGCAGCACCGCTGGCAAGATTGACCTGCTGGGTGG	5994	C>G	
561	C	1	Exon	GAATATATCCGGCCCTTCGCCAGCCTGGTGACAGGCCGGA	5995	G>A	
561	E	+1	Intron	CAGGGCTCCACACATACTCCCTGGCCACCACGCCCTCCTCTC	5996	T>C	
561	E	+2	Intron	ACTCCGTAGTTACCAGGTTGCCCTCTTGACGACTGGAAA	5997	G>C	
561	E	1	Exon	AGCTGAGCTGCCCTCACCAGCGGGGAAATACCTCTACGTC	5998	C>T	Ala > Val
561	G	+2	Intron	GGGTGGGGAGGGTTTGTAGGCCCTAACGCAGCAGGAGGACCG	5999	G>A	
561	G	+3	Intron	GTGGGAGGGTTTGTAGGCCCTAACGCAGCAGGAGGACCGGC	6000	C>T	
561	G	-1	Intron	GCCAGGGCTGCTCCCTGAACGCCCTCCGTTCCCTCTGTCCC	6001	G>A/C	
561	H	-1	Intron	GCTCAACCTCGGGCAGCCCGCGAGCCAGCTCTGCTGTCCAC	6002	G>A	
561	H	-2	Intron	GGCTCCCATTTGCAGGACCGCGGGGGCTCACCTCGGGCAGC	6003	G>*	
561	H	1	Exon	TCACCCAGCCGCATCTGCCACAGCCACAGGGCACCCCGGT	6004	A>G	
561	J	1	Exon	CTGGAAGATGGGGGAAAGGAGCGGGCCAGCGGCACGTCCCA	6005	G>A	
561	M	+1	Intron	AAATAGGTAAAGCGCAAAACCCCTATTGACCTTCCCTGTGC	6006	C>A	
561	M	+2	Intron	TATGCCAAAGTCATGTAAATGTTGACCAGTGATTTTCTTG	6007	G>A	
561	M	+3	Intron	GCCAAAGTCATGTAAATGTTGACCAGTGATTTTCTTGGGC	6008	G>A	
561	M	+4	Intron	TTGGCAAAAGCCACCCCTACGAAACAGGACTGCCAGTAGTC	6009	G>A	
561	P	+1	Intron	TAAGCAACCTATTAGCCTTTTAATCTCTGTCCCGTTCT	6010	T>C	
561	P	1	Exon	GTGTTTTAGGGGAGCTGAATGGGCAGAAAGGCTGTGCC	6011	T>C	
561	X	-1	Intron	TCTGTGAGGGTAAGGAACACATCTGCTCTGTACTACTTA	6012	A>T	
561	X	-2	Intron	TCTCTCTGTAGGGTAAGGAACACATCTGCTCTGTTACTA	6013	A>C	
561	X	-3	Intron	GACACCCAGATTTTCAGGCAATCAAGTTCTTTCTTGCCCTCAG	6014	T>A	
561	Y	+1	Intron	ATCTGGGGCCCTGGAGGGAGCGGGGCTGGCCAGGGAGGAAC	6015	C>G	
561	Y	+2	Intron	TGAGGCACCCAGTGATGTCATCCACATATCTGCTGTTAT	6016	C>T	
561	Y	+3	Intron	CCAGTGATGTCATCCACTATCTGCTGTTATCTCTGCTT	6017	A>G	
561	Y	-1	Intron	TACCAAGTCTCTAAACATGGGGGCACCATCTCACATGTCCT	6018	G>C	
561	Y	-2	Intron	TCCAATTGGCGAGAAAGTCCGTTGCTTTTAAAGACACAGA	6019	G>A	
561	Y	-3	Intron	CTCCAATTGGCGAGAAAGTCCGTTGCTTTTAAAGACACAG	6020	C>T	
570	C	-1	Intron	TTAACCACTTGACCGTATATGTTTTCATCTGAAGACTG	6021	G>C	
570	C	1	Exon	TTAGGTTAAAGATCGAGGTCGGGAAGCCACTAGGAGATTTT	6022	C>T	Pro > Leu
570	C	2	Exon	AGGCGGCTTGTCTTTGTGGTCTCTCTGTGGCAAGAGCGG	6023	T>C	Val > Ala
570	C	3	Exon	CTTTTGTGTCCTCTCTGTGGCAAGAGCGTTTTCATCACC	6024	G>A	Gly > Ser

570	C	4	Exon	GAGGCGAGTGCCTTTCACAGAGCATGTTCAAGATACTGACGTA	6025	C>T	
570	F	+1	Intron	GTTGTGATTACGAATATAGTCTCACACGCGAGTCGTCCC	6026	T>C	
570	F	-1	Intron	AAGAAATCTTTCCAGATTCCGTTGTCTCTAAACTGAAGAG	6027	C>T	
570	F	1	Exon	ATGTTCTTTGTCAATGTGCTCGGCCCTTGCTGCAGGTAAGAG	6028	G>A	
570	J	1	Exon	TATTGAACTATTACTTTTTTCTTCTGCTGCTATTCAAGG	6029	T>C	
581	F	+1	Intron	TGTGGCCACTTGTCTGTACGATTGTTGGTTGGCTTGT	6030	G>C	
581	F	+2	Intron	CTTTGCTGTTACAGATTGTTGGTTGGCTTGTATTCCCTG	6031	G>T	
581	F	-1	Intron	TGTACTATTGGCCTCAGGCAATCCACCCTCAGCCCCGAAA	6032	A>G	
698	B	-1	Intron	AGCCTTGCTATTGGCATCAGCTCTTTATTTTTTTAAAAAAT	6033	C>T	
698	B	1	Exon	CGGGGCCCTGGGGGACACTGCCAGGGCCTGCCATGCTCAT	6034	G>A	
698	E	1	Exon	AGCCATGGGCATGCAAAATGAGAAAAAGCAATAATGTAAGTTA	6035	G>A	Arg > Lys
698	I	+1	Intron	GTCGCGCTGCAAGGTTAGTCACTGTGGGTTGCCATTCTA	6036	A>G	
698	I	+2	Intron	GTTATTGATGGGCCACAGACTTTGGGAAGAACAGACGAGTTG	6037	T>C	
698	I	-1	Intron	TGATGCTGATACGGGATCTCTGTATCTCTCTCTCTGTG	6038	T>C	
702	A	-1	Intron	TTTATTAGACACACTTTTCCGGCAGCTGCCAGGGAGAGAGAC	6039	G>A	
702	B	+1	Intron	ACCTGTCGTGAGAGTGGGTGTGTGGCCAGGGTGAGGAGCGG	6040	T>C	
702	B	+2	Intron	GGAGGTGGCGCGGTGCCAGGGTGAGGAACGGGGTCTCCGT	6041	G>C	
702	B	+3	Intron	GGGTGCGTGGCCAGGGGTAGGGAACAGGGGTCTCCGTGAGGT	6042	G>C	
702	B	-2	Intron	GTGCCAGAGTCAGGGCTCCCAACCCTTGCGGATGCTCGGGAT	6043	A>G	
702	C	1	Exon	GCCCCAGACGGCCAGCACCCAGCGGAGGTCAGCCGGGCCGAGC	6044	G>A	Ala > Thr
702	D	-1	Intron	GGGATGCCCTCGATGCCGGCTGCCAGAGGGAATTCGCAGG	6045	G>A	
702	D	1	Exon	CCTCGTAGGGGAGGCCCGTAGCGGCAGCGGGTCACCACCGGG	6046	C>T	Arg > His
702	F	-1	Intron	GCCCCGTGCCCGCTGCCCAAGGGCCCCCGCTCCCAAGCCAC	6047	G>*	
702	F	1	Exon	GACGCGGTGCCCCAGATCCGGGTGAAGCTTTCTTCTTCAA	6048	G>C	Arg > Pro
702	I	1	Exon	TGTGTGAGACTCACAGGCCGATGATCTGTGGCTGCGGGC	6049	G>A	Asp > Asn
702	I	3	Exon	CCCAGAGGTGCAITGAGCAGAGCCTCGTAACCGTCTCCGAGC	6050	G>A	Val > Ile
722	AA	+2	Intron	CACGCAGTACAGATAATGCCATCTAGTATACATCTGCCCTG	6051	A>G	
722	AA	-1	Intron	GGATGTCTTTTAATGTGGCAATATGAAATTAACCATGCATG	6052	A>G	
722	AA	-2	Intron	GCCACACACACCTGGCCAGGTTGTTTATTTAATGAAGGA	6053	C>T	
722	AA	-3	Intron	CTCAGGTGATCCATCCGCTGGGACTCCCAAAGTGTGAGA	6054	C>G	
722	AA	-4	Intron	CTGACCTCAGGTGATCCATCGGCTCGGACTCCCAAAGTGC	6055	C>T	
722	C	1	Exon	GGTGGAGGAGATTAGAAACAGTATTGATAAATAACTCAAT	6056	G>C	Ser>Thr
722	F	+1	Intron	AAGTGAGTAATGGAGACTCCGCTCTTTGTTAAATCATGTTT	6057	G>A	
722	G	-1	Intron	AAAAATGCTAACACACTATGATGTGATGTGCTAACTTATGTT	6058	T>C	
757	A	+1	Intron	ACTTTTGTTAGAGCCCTCCGTAATAATATACATCTGTGATT	6059	G>C	
757	A	+2	Intron	GAGTTGCTTAAATAGACTCCGGCCCTCACCAATAGTCTCT	6060	C>T	
757	A	+3	Intron	AGGCCCAGCCCTCAGAAACCCTTCAGTGTACATTTTGTGG	6061	C>T	

757	A	+4	Intron	ACCAAGCCAATGTTATAGAC <u>G</u> TTTGACTGATTGTGAAA	<u>6062</u>	G>C	
757	A	+5	Intron	GACTGATTGTGAAAGGAG <u>G</u> GGGGAAGAGGAGAAAGATC	<u>6063</u>	G>A	
757	A	+6	Intron	GCTAGTGTATTCTCTCACA <u>G</u> TGCCAGGAAGAGTGGTTT	<u>6064</u>	A>G	
757	A	-1	Intron	CCGAGCCGGGGGGCGCTGTGCAGCGCTCGGGCCAGGCCGG	<u>6065</u>	G>A	
757	A	2	Exon	TTGCACGAGTTCCGCCCGCT <u>G</u> GTGGAGTACGGCTGCCACGG	<u>6066</u>	G>C	
757	A	4	Exon	CTCACCTTCCTCATCGACCC <u>G</u> GGCCCGCTCCGCTACCCCGA	<u>6067</u>	G>C	
757	A	5	Exon	AGCCGGAGAAACCGGCCAGC <u>G</u> GTGATCACCAGCGGTGGAT	<u>6068</u>	C>T	

Please replace Table 11A on pages 189-191 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 11A: ASA PRIMERS

SNP	ASA Type	RFLP Enzyme	ASO Primer1	SEQ ID NO:	ASO Primer2	SEQ ID NO:	Base change	AA change
214_B_1	RFLP	NdeII					C>T	
214_C_-1	ASO		ACCTCAACCCAGGCGTT	6069	CACCTCAACTCAGGCGTTTG	6080	C>T	
214_E_+1	RFLP	PvuII					T>C	
214_E_+2	RFLP	MspI					G>C	
214_E_-1	RFLP	AvaI					C>T	
214_E_1	ASO		CTCTCTCTGTGAGTGTC	6070	CTCTCTCTTTGAGTGTCTGG	6081	G>T	Val>Leu
214_E_2	ASO		ACCTCAACCCAGGCGTTT	6071	CCACCTCAACTCAGGCGTTT	6082	C>T	
214_E_3	ASO		TGCTTGACCCCAATCC	6072	GTGCTTGACCTCCAATCCG	6083	C>T	Pro>Ser
422_E_2	ASO		TCATACTCGTCTCTGGC	6073	TATTCATACTCATGCTCTGGCT	6084	G>A	
436_A_+2	ASO		TGTTTAAAGCCACAGCCT	6074	CTGTTTAAAAACACACAGCCTGG	6085	G>A	
436_A_1	ASO		CCCTCGGTTCCACCGTC	6075	GCCATGGCGTGTGCTGC	6086	G>T	Gly>Cys
436_A_2	ASO		GTGCAACTGCTCATCCTG	6076	CGTGCAACTGTTTCATCCTGG	6087	C>T	Leu>Phe
436_C_+1	RFLP	DraII					G>A	
436_C_-1	RFLP	MwoI					C>T	
436_D_1	RFLP	DraII					G>A	
436_E_1	RFLP	AvaI					C>T	
436_G_1	ASO		GCAGGACACAGTTTCCAGGA	6077	CAGGACACGCGTTTCCAG	6088	A>G	Ser>Gly
436_K_+1	RFLP	AlwNI					C>G	
436_K_-2	ASO		CTCAGGAAGGGGCACGCA	6078	CTCAGGAACGGGCACGCA	6089	G>C	
436_L_-1	ASO		CTCCCTCCCGCCTGCCAC	6079	CTCCCTCCTGCTGCCAC	6090	C>T	
436_L_-3	RFLP	XmaI					C>T	
436_L_1	RFLP	HhaI					T>C	
454_B_1	RFLP	Bstul					T>C	Val>Ala
454_E_-1	RFLP	PstI					C>T	
454_E_1	RFLP	HpaII					G>A	Gly>Arg
454_E_2	RFLP	NlaIII					C>T	His>Tyr
454_E_3	RFLP	BanI					C>T	
454_F_-2	ASO		CCCTCGGTCCCGACCGTC	6091	CCCTCGGTTCCACCGCTC	6107	C>T	
454_G_-1	RFLP	BstYI					A>T	
454_H_1	ASO		CATCACTGCCGTCCCAAA	6092	CCATCACTGCCATCCCAAT	6108	G>A	Arg>His
454_H_2	ASO		CAGTTTCCGTGCGCTTGA	6093	CAGTTTCCATCGCCTTGACG	6109	G>A	Arg>His
454_K_1	RFLP	AlwNI					G>A	Arg>Gln

454_L_-1	RFLP	Earl					C>T	
454_M_+1	ASO		CCAAGACACGGAGAGATT	6094	ACCAAGACATGAGAGATTCC	6110	C>T	
454_M_1	RFLP	MspAI					A>G	Ala>Thr
454_M_2	ASO		CATCGACACTTACTCCAG	6095	CATCGACAGTTACTCCAG	6111	C>G	Thr>Ser
454_O_1	RFLP	PvuII					A>G	Gln>Arg
454_O_3	RFLP	HhaI					A>C	Glu>Ala
454_O_5	ASO		ACTTGGCCATCCTGCCCAG	6096	ACTTGGCCAACCTGCCCAG	6112	T>A	Ile>Asn
454_O_6	RFLP	MboII					A>G	
515_A_1	ASO		GCGGATCCGCATCTTCT	6097	TGCGGATCCACATCTTCTGG	6113	G>A	Arg>His
515_A_2	ASO		GGAAGATGACAGGTGAGC	6098	AGGAAGATAACAGGTGAGCC	6114	G>A	MET>Ile
515_A_3	RFLP	HaeIII					G>C	MET>Ile
515_A_4	RFLP	Bsu36I					G>A	Val>Ile
515_A_5	RFLP	BsmI					C>G	Ile>MET
515_A_6	RFLP	BsmI					T>C	
515_A_7	RFLP	XcmI					A>G	
561_B_+1	ASO		AGAAITGGCCGTTGGCTG	6099	GAGAAITGGCTGTTGGCTGC	6115	C>T	
561_B_1	ASO		CACGCTGGCAAGATTGAC	6100	CACGCTGGGAAGATTGAC	6116	C>G	
561_C_1	RFLP	MwoI					G>A	
561_E_+1	RFLP	MspI					T>C	
561_E_1	ASO		CCTCACGGCGGGAAAT	6101	CCCTCACGGGTGGGAAATAC	6117	C>T	Ala>Val
561_H_1	ASO		CATCCTGCCACACAGCCACAG	6102	ATCCTGCCCGCAGCCACA	6118	A>G	
561_J_1	ASO		GGAAGGAGGCGGCCCA	6103	GGAAGGAGACGGGCCAG	6119	G>A	
561_M_+1	ASO		CGCAAAACCCCTATTGAC	6104	GCGCAAAACCACTATTGACC	6120	C>A	
561_P_1	ASO		GAGCTGAACGGGCAGAA	6105	GGAGCTGAATGGGCAGAAAG	6121	T>C	Arg>Trp
561_X_-3	ASO		ATTTTCAGGCATCAAGTTCTTTC	6106	ATTTTCAGGCAACAAGTTCTTCT	6122	T>A	
561_Y_+1	RFLP	BsrBI					C>G	
561_Y_-1	RFLP	Fnu4HI					G>C	
570_C_1	RFLP	MspI					C>T	Pro>Leu
570_C_2	ASO		GCTTTTGTGGTCTCTCTG	6123	CTTTTGTGGCCTTCTCTCT	6135	T>C	Val>Ala
570_C_3	ASO		CTTTCACACAGCATGTTCAAG	6124	GCTTTCACAGATATGTTCAAGA	6136	G>A	Gly>Ser
570_C_4	RFLP	AflIII					C>T	
570_F_1	RFLP	DdeI					G>A	
581_F_+2	ASO		AGATTGTTGGTTGGCTT	6125	TCAGATTGTTCTGTTTGGCTTG	6137	G>T	
698_E_1	ASO		CATGCAAAATGAGAAAAAGCAAT	6126	GGCATGCAAAATGAAAAAAGCAAT	6138	G>A	Arg>Lys
698_L_+1	ASO		CCCCACAGGTGACTAACCTT	6127	CCCACAGGGCGACTAACCC	6139	A>G	
702_A_-1	ASO		ACTTTTCCGGCAGCTGC	6128	ACTTTTCCGTCAAGCTGCCC	6140	G>A	
702_B_+1	ASO		AGGTGGGTGTGTGCCAG	6129	GGTGGGTGCGTGCCA	6141	T>C	

702_B_+3	ASO		AGGGTGAGGAACGGGGT	6130	AGGGTGAGCAACGGGGT	6142	G>C	
702_C_1	RFLP	HaeII					G>A	Ala>Thr
702_D_1	RFLP	HhaI					C>T	Arg>His
702_F_1	RFLP	NciI					G>C	Arg>Pro
702_I_1	RFLP	XcmI					G>A	Asp>Asn
702_L_3	RFLP	DpnII					G>A	Val>Ile
722_C_1	ASO		GATTAGAAACAGTATTGATAAA	6131	GATTAGAAACACTATTGATAAA	6143	G>C	Ser>Thr
722_F_+1	RFLP	Tth111					G>A	
722_G_-1	ASO		AACCACTATGATTGTAGTTGCTA	6132	CAACTATGACTGTAGTTGC	6144	T>C	
757_A_+4	RFLP	HpyCH4IV					G>C	
757_A_-1	ASO		GCTGTGCGCAGCGCTC	6133	CGCTGTGCACAGCGGCTCG	6145	G>A	
757_A_2	ASO		GCGCCGCTGGTGGAGTA	6134	GCGCCGCTCGTGGAGTA	6146	G>C	
757_A_4	RFLP	Sau96I					G>C	
757_A_5	RFLP	Cac8I					C>T	

Please replace Table 11B on page 194 with the following table:

TABLE 11B: EPA PRIMERS

SNP	Primer Seq. (5'-3')	SEQ ID NO:
436_K_-2	TTATTCTTTGCGTGCCC	<u>6147</u>
436_K_-2	ACCTTCCCTTCTCCAAGACC	<u>6148</u>
436_K_-2	ATTCCAGGCTTCTCAGGAA	<u>6149</u>
436_K_-2	CGCCTGAGTTTAGCATAGGG	<u>6150</u>
454_F_-2	CATGGGCTCCCTCGGT	<u>6151</u>
454_F_-2	CCGGGGAAGTCGATATTGTT	<u>6152</u>
454_F_-2	CATGGGCTCCCTCGGT	<u>6153</u>
570_C_2	GCGGTCTTGCTTTTGTGG	<u>6154</u>
570_C_2	TTACTCTGGCGCTCTCCACT	<u>6155</u>
570_C_2	CGGTCTTGCTTTTGTGG	<u>6156</u>
698_I_+1	AGAATGGCAACCCACAGG	<u>6157</u>
698_I_+1	GCTGGTTCTCACGCTGCATATT	<u>6158</u>
698_I_+1	GTAGAATGGCAACCCACAGG	<u>6159</u>